

From: Mertz, Prema  
Sent: Monday, October 31, 2005 3:22 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/748,484

Please search SEQ ID NO:2 and any 6 amino acids of SEQ ID No:2 with protein databases.

Please search USGPUB databases with SEQ ID NO:2.

Thanks.

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aa

Mej 176

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Date completed: \_\_\_\_\_

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

#### Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

#### Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ Other CAF

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 2, 2005, 18:32:00 ; Search time 40 Seconds

(without alignments)  
423.354 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 910  
Sequence: 1 MKASSLAFSLSLAFAFLYLLMT.....AVVKALGELDIILQNMETE .176

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156.5	17.2	178	2 A38580	interleukin-10 pre
2	155	17.0	170	1 QOBR2	BCRF1 protein - hu
3	155	17.0	175	2 I46591	interleukin 10 - p
4	147.5	16.2	179	2 A48558	interleukin 10 hom
5	144	15.8	178	2 A34853	interleukin-10 pre
6	136	14.9	178	2 JN0475	interleukin-10 pre
7	94.5	10.4	567	2 JCS538	Rab geranylgeranyl
8	94.5	10.4	567	2 A45977	Rab geranylgeranyl
9	93.5	10.3	809	2 S64594	probable beta-adap
10	85	9.3	140	2 F83128	probable transcrip
11	81.5	9.0	646	2 T33346	hypothetical prote
12	81	8.9	1062	2 S46367	protein kinase CDC
13	80	8.8	542	2 T19925	hypothetical prote
14	76.5	8.4	502	2 AD3160	hypothetical prote
15	76.5	8.4	553	2 B90153	2-isopropylmalate
16	76	8.4	523	2 S64826	probable membrane
17	76	8.4	917	2 T21870	hypothetical prote
18	75	8.2	276	2 B71517	probable synchocy
19	75	8.2	726	2 T48023	ATP-dependent RNA
20	75	8.2	729	2 H84912	probable pre-mRNA
21	74.5	8.2	121	2 E83640	hypothetical prote
22	74.5	8.2	1047	2 D71302	probable exonuclea
23	74	8.1	682	1 H69819	ATP-dependent DNA
24	73.5	8.1	449	2 B71917	udp-n-acetylurama
25	73.5	8.1	653	2 D87602	sensory box histid
26	73.5	8.1	729	2 F97321	membrane export pr
27	73.5	8.1	794	2 S33945	late protein, 100K
28	73.5	8.1	794	2 A98211	hypothetical prote
29	73.5	8.1	794	2 C86057	hypothetical prote

30	73	8.0	471	2 B38637	Ras inhibitor (clo
31	73	8.0	563	2 D90531	exonuclease ABC s
32	73	8.0	614	2 B83880	hypothetical prote
33	73	8.0	1008	2 D84434	probable receptor-
34	72.5	8.0	261	2 H98213	transcription repr
35	72.5	8.0	388	2 T00641	hypothetical prote
36	72.5	8.0	409	2 A54750	TNF receptor asoc
37	72.5	8.0	447	2 T20552	hypothetical prote
38	72.5	8.0	481	2 S38682	YmbL protein - Bac
39	72.5	8.0	1101	2 T33153	hypothetical prote
40	72.5	8.0	2182	2 T28634	variant-specific s
41	72.5	8.0	2581	2 AP2545	conserved hypotet
42	72	7.9	255	2 F81833	hypothetical prote
43	72	7.9	255	2 E81197	conserved hypotet
44	72	7.9	279	2 A70081	hypothetical prote
45	72	7.9	351	2 S74651	hypothetical prote

#### ALIGNMENTS

RESULT 1  
A38580  
interleukin-10 precursor - human  
N:Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10  
C:Species: Homo sapiens (man)  
C:Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #ext\_change 09-Jul-2004  
C:Accession: A38580; GO1539; S49110; 137890  
R:Vieth, P.; de Maal-Malefyt, R.; Dang, M.N.; Johnson, K.E.; Kastelein, R.; Fiorentino, Proc. Natl. Acad. Sci. U.S.A. 88, 1172-1176, 1991  
A>Title: Isolation and expression of human cytokine synthesis inhibitory factor cDNA cl  
A:Reference number: A38580; MUID:91142134; PMID:1847510  
A:Accession: A38580  
A:Molecule type: mRNA  
A:Residues: 1-178 <VIB>  
A:Cross-references: UNIPROT:P22301; GB:M57627; NID:g186270; PID:AAA63207.1; PID:g18627  
R:Rindor, W.T.; Syro, R.; Tsaribopolos, A.; Zhang, R.; Durkin, J.; Baldwin, S.; Pallwal  
Biochemistry 32, 8807-8815, 1993  
A>Title: Disulfide bond assignments and secondary structure analysis of human and murin  
A:Reference number: A48693; MUID:93372085; PMID:8364028  
A:Contents: annotation; disulfide bonds in recombinant protein  
R:Sanjanwala, B.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: G07695  
A:Accession: G01539  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-178 <SAN>  
A:Cross-references: EMBL:U06720; NID:g1041812; PID:AAA80104.1; PID:g1041813  
R:Kube, D.; Platzer, C.; von Knechten, A.; Straub, H.; Hafner, M.; Tesch, H.  
submitted to the EMBL Data Library, March 1994  
A:Description: Isolation of the human interleukin-10-promoter. Characterization of the  
A:Reference number: S49110  
A:Accession: S49110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6, 'PVAMSS' <KUB>  
A:Cross-references: EMBL:X78437; NID:g1167482  
R:Platzer, C.; Volk, H.D.; Platzer, M.  
DNA Seq. 4, 399-401, 1994  
A>Title: 5' noncoding sequence of human IL-10 gene obtained by oligo-cassette PCR walki  
A:Reference number: I37890; MUID:95143580; PMID:7841462  
A:Accession: I37890  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <PLA>  
A:Cross-references: EMBL:X73536; NID:g452395; PID:CAA51942.1; PID:g580177  
C:Gene: GDB:1110; IL-10  
A:Cross-references: GDB:128636; OMIM:124092  
A:Map position: 1q31-1q32  
A:Introns: 55/3; 75/3; 126/3; 148/3  
C:Superfamily: interleukin-10

C:Keywords: cytokine; glycoprotein; lymphokine; T-cell  
F:1-18/Domains: signal sequence #status predicted <S>  
F:19-178/Product: interleukin-10 #status predicted <M>  
F:30-126,80-132/Disulfide bonds: #status experimental  
F:134/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 17.2%; Score 156.5; DB 2; Length 178;  
Best Local Similarity 27.4%; Pred. No. 7.9e-08;  
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 5;  
QY 22 STGLTNLNGSCV-----IATNLOEIRNGFSDIRGSVOAKGNDIRLRRTESLQDTKP 76  
DB 19 SPGQGTQSENSCTHPGMLPMLRLDRDAFSKVFQWKD-QLD-NLLKESLLEDFKG 76  
QY 77 ANRCLLHLRLYLDRVFNKVGTPDHTLRKISLANSFLTIKKDLRCHAMTCHGE 136  
DB 77 YLGCALSEMDIPLYEEVWPAQENODPDIKAHVNSLGEKTLRLRCHRFPLC---E 133  
QY 137 BAKKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173  
DB 134 NKSRAVEQVKNAFNKLQ-EKGIYKAMSEFDIFINYIE 169

## RESULT 2

QOBER2  
BCRF1 protein - human herpesvirus 4 (strain B95-8)  
C:Species: human herpesvirus 4, Epstein-Barr virus  
C:Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 09-Jul-2004  
C:Accession: A03741; S32974  
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
Mol. Biol. Med. 1, 21-45, 1983  
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus  
A:Reference number: A33065; MUID:85035713; PMID:6092825  
A:Accession: A03741  
A:Molecule type: DNA  
A:Residues: 1-170 <BAN>  
A:Cross-references: UNIPROT:P03180; EMBL:V01555; NID:959074; PIDN:CAA24863.1; PID:959076  
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H  
Nature 310, 207-211, 1984  
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A:Reference number: A03794; MUID:84270667; PMID:6087149  
A:Contents: annotation; protein coding region  
C:Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 1; Length 170;  
Best Local Similarity 28.9%; Pred. No. 1e-07; Indels 6; Gaps 4;  
Matches 39; Conservative 29; Mismatches 61;  
QY 39 LOEIRNGFSDIRGSVOAKGNDIRLRRTESLQDTKPANRCLLRLYLDRVFNKY 98  
DB 34 LRDLADAFSRVKTFFQTD-EVD-NLLKESLLEDFKGLGQALSEMIQFLSEVMPQ 91  
QY 99 QTPDHTLRKISLANSFLTIKKDLRCHAMTCHGEAMKYSQILSHFEKLEPQAAV 158  
DB 92 ENODEAKDHNVSLOENKTLRLRCHRFPLC---ENKSKAVESQIKVAFKQ-EKGI 147  
QY 159 VKALGELDILLQWME 173  
DB 148 YKAMSEFDIFINYIE 162

## RESULT 3

146591  
interleukin 10 - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: 146591  
R:Blanchard, G.; Gianello, P.; Germans, S.; Baetscher, M.; Sachs, D.H.; Leguern, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 2800-2804, 1995  
A:Title: Molecular identification of porcine interleukin 10: regulation of expression in  
A:Reference number: 146591; MUID:95224028; PMID:7708727  
A:Accession: 146591  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-175 <BLA>  
A:Cross-references: UNIPROT:Q29055; GB:L20001; NID:9309792; PIDN:AAA74410.1; PID:9309793  
C:Genetics:  
A:Gene: IL-10  
C:Superfamily: interleukin-10

Query Match 17.0%; Score 155; DB 2; Length 175;  
Best Local Similarity 27.0%; Pred. No. 1.1e-07;  
Matches 48; Conservative 34; Mismatches 78; Indels 18; Gaps 6;  
QY 1 MKASLAFSLSAAFYLLMTPSTGLTNLNGSCV-----IATNLOEIRNGFSDIRGSVOA 55  
DB 1 MPSSALYLCI-----FLAGVAASIKSEN--SCIFPSTLPHMLRELRAAGPVKSPQT 53  
QY 56 KQGNIDIRLRRTESLQDTKPANRCLLRLYLDRVFNKVGTPDHTLRKISLANS 115  
DB 54 KDQMGD-LLLTGSLLLEDFKGLGQALSEMIQFLSEVMPKASDGSDIKEHVSLSGEK 111  
QY 116 FLTIKKDLRCHAMTCHGEAMKYSQILSHFEKLEPQAAVVKALGELDILLQWME 173  
DB 112 LKTLRLRCHRFPLC---ENKSKAVESVSAFSKLQ-EKGIYKAMSEFDIFINYIE 165

## RESULT 4

A48558  
interleukin 10 homolog - equine herpesvirus 2  
N:Alternate names: hypothetical protein E7  
C:Species: equine herpesvirus 2  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A48558; S55664  
R:Rode, H.J.; Jansen, W.; Rosen-Wolff, A.; Bugert, J.J.; Thein, P.; Becker, Y.; Darat,  
Virus Genes 7, 111-116, 1993  
A:Title: The genome of equine herpesvirus type 2 harbors an interleukin 10 (IL10)-like g  
A:Reference number: A48558; MUID:93227565; PMID:8385838  
A:Accession: A48558  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-179 <ROD>  
A:Cross-references: UNIPROT:Q89451; GB:S59624; NID:9299468; PIDN:AAE26148.1; PID:9299469  
A>Note: sequence extracted from NCBI Backbone (NCBI:129334, NCBI:P:129335)  
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S5564; MUID:95302501; PMID:7783207  
A:Accession: S5564  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-179 <TEB>  
A:Cross-references: GB:U20824; NID:9695172; PIDN:AC13857.1; PID:9695242  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995  
C:Superfamily: interleukin-10

Query Match 16.2%; Score 147.5; DB 2; Length 179;  
Best Local Similarity 31.9%; Pred. No. 6e-07;  
Matches 44; Conservative 24; Mismatches 59; Indels 11; Gaps 6;  
QY 39 LOEIRNGFSDIRGSVOAKGNDIRLRRTESLQDTKPANRCLLRLYLDRVFNKY 98  
DB 41 LHELRAAFSRVKTFFQMD-QLD-NMLLDGSLLEDFKGLGQALSEMIQFLSEVMP-- 96  
QY 99 QTPDHTLR---KISLANSFLTIKKDLRCHAMTCHGEAMKYSQILSHFEKLEPQ 155  
DB 97 QAEHSTQEDKDNVSLSEKTLRLRCHRFPLC---ENKSKAVESVSAFSKLQ-E 152  
QY 156 AAVVKALGELDILLQWME 173  
DB 153 KGVYKAMSEFDIFINYIE 170

## RESULT 5

A34853  
interleukin-10 precursor - mouse

N/Alternate names: cytokine synthesis inhibitory factor (CSIF); IL-10  
 C/Species: Mus musculus (house mouse)  
 C/Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 09-Jul-2004  
 C/Accession: A34853; 156136  
 R/Moore, K.W.; Vieira, P.; Fiorentino, D.F.; Trounstein, M.L.; Khan, T.A.; Mosmann, T.R.  
 Science 248, 1230-1234, 1990  
 A/Title: Homology of cytokine synthesis inhibitory factor (IL-10) to the Epstein-Barr vi  
 A/Reference number: A34853; MUID:9023182; PMID:2161559  
 A/Accession: A34853  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-178 <MO>  
 A/Cross-references: UNIPROT:P18933; GB:M37897; NID:g198288; PIND:AAA39274.1; PID:g198288  
 R/Kim, J.M.; Brennan, C.I.; Copeland, N.G.; Jenkins, N.A.; Khan, T.A.; Moore, K.W.  
 J. Immunol. 148, 3618-3623, 1992  
 A/Title: Structure of the mouse IL-10 gene and chromosomal localization of the mouse and  
 A/Reference number: 156136; MUID:92268508; PMID:1350294  
 A/Accession: 156136  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-178 <RES>  
 A/Cross-references: GB:M84340; NID:g198291; PIND:AAA39275.1; PID:g198292  
 C/Genetics:  
 A/Gene: IL10  
 A/Introns: 55/3; 75/3; 126/3; 148/3  
 C/Superfamily: Interleukin-10  
 C/Keywords: cytokine; lymphokine; T-cell

Query Match 15.8%; Score 144; DB 2; Length 178;  
 Best Local Similarity 31.1%; Pred. No. 1.3e-06;  
 Matches 42; Conservative 19; Mismatches 68; Indels 6; Gaps 4;

QY 39 LQIRNGSPDIRGSVOAKGONIDIRILRTESLODPKPNRCCLRLRLYLDRVFNKY 98  
 Db 41 LLELRATFSOVKTFPTQKD-QLD-NILIDSLMDPKGYLGCQALSMIQLYLVEMPOA 98  
 QY 99 QPDEHYTLRKISSIANSFLTIKDLRLCHAMTCHGCEAMKYSQILSHPEKLEPOAAV 158  
 Db 99 EKKGPEIKELHNLGELKTLRLRLRCHRFPC---ENSKAVEQVKSDFNKLQDQ-GV 154  
 QY 159 VKALGELDIILQWME 173  
 Db 155 YKAMNEPDIPIICIE 169

RESULT 6  
 JN0475  
 Interleukin-10 precursor - rat  
 N/Alternate names: cytokine synthesis inhibitory factor  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C/Accession: JN0475; JCI357; S36021  
 R/Feng, L.; Tang, W.W.; Chang, J.C.C.; Wilson, C.B.  
 Biochem. Biophys. Res. Commun. 192, 452-458, 1992  
 A/Title: Molecular cloning of rat cytokine synthesis inhibitory factor (IL-10) cDNA and  
 A/Reference number: JN0475  
 A/Accession: JN0475  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-178 <FEN>  
 A/Cross-references: UNIPROT:P29456  
 R/Goodman, R.E.; Oblak, J.; Bell, R.G.  
 Biochem. Biophys. Res. Commun. 189, 1-7, 1992  
 A/Title: Synthesis and characterization of rat interleukin-10 (IL-10) cDNA clones from c  
 A/Reference number: JCI357; MUID:93080542; PMID:1280414  
 A/Accession: JCI357  
 A/Molecule type: mRNA  
 A/Residues: 1-'P', 3-64, 'L', 66-178 <GOO>  
 A/Cross-references: GB:I02926; NID:g204903; PIND:AAA41425.1; PID:g204904  
 R/Feng, L.  
 submitted to the EMBL Data Library, July 1991  
 A/Reference number: S36021  
 A/Accession: S36021

A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-178 <FE2>  
 A/Cross-references: EMBL:X60675; NID:g296620; PIND:CAA43090.1; PID:g296621  
 C/Species: Homo sapiens (man)  
 C/Accession: J05538  
 R/Song, H.-J.; Rossi, A.; Cecil, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.  
 Biochem. Biophys. Res. Commun. 235, 10-14, 1997  
 A/Title: The genes encoding geranyl transferase alpha-subunit and transglutaminase  
 A/Reference number: J05538; MUID:97339427; PMID:9196026  
 A/Accession: J05538  
 A/Molecule type: DNA  
 A/Residues: 1-567 <SON>  
 A/Cross-references: UNIPROT:Q92696  
 C/Comment: This protein is involved in cutaneous disease. The gene of this enzyme is po  
 C/Genetics:  
 A/Gene: Rabgga  
 A/Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 413/  
 C/Keywords: transferase

Query Match 10.4%; Score 94.5; DB 2; Length 567;  
 Best Local Similarity 25.8%; Pred. No. 0.34;  
 Matches 49; Conservative 26; Mismatches 82; Indels 33; Gaps 9;

QY 1 MKASSLAFLSAAYFLMTPTGTLKTLNLSGVATNLOE--IRNGFSD---IRGSVOA 55  
 Db 304 LPAASLNDQLPQHRTFVITAGDVOK-----ECVLLKRGEGWCRCRSTTDEQLFRCELSV 358  
 QY 56 KQGNIDIRILRTESLODPKPNRCCLRLRLYLDRVFNKYQT-----PDH 103  
 Db 359 EKSTVLOSLESCKEQLPEPKKWCILITLLMRALDPLLYEKETQLYQYOTLKAUVMR 418  
 QY 104 YT-----LRKISSIANSFLTIK---KDLRLCHAMTCHGCEAMKYSQI-LSH--FEKL 152  
 Db 419 ATTIIDLRSGFLIENSVLKNIEVAVRYLHLAHMDLVTLCHLEQLLVTHDLSNRRLRTL 478  
 QY 153 EPQAAVVKAL 162  
 Db 479 PPALALRLCL 488

RESULT 8

A45977  
Rab geranylgeranyl transferase component B alpha subunit - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A45977  
R:Armstrong, S.A.; Seabra, M.C.; Sudhof, T.C.; Goldstein, J.L.; Brown, M.S.  
J. Biol. Chem. 268, 12221-12229, 1993  
J>Title: cDNA cloning and expression of the alpha and beta subunits of rat Rab geranylge  
A:Reference number: A45977; MUID:93280201; PMID:8505342  
A:Accession: A45977  
A:Status: Preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-567 <ARM>  
A:Cross-references: UNIPROT:Q06602; GB:S62096; NID:G385474; PIDN:AA827018.1; PID:G385475  
A:Experimental source: brain  
A>Note: sequence extracted from NCBI backbone (NCBIN:133369, NCBI:P:133370)  
  
Query Match 10.4%; Score 94.5; DB 2; Length 567;  
Best Local Similarity 24.2%; Pred. No. 0.34;  
Matches 46; Conservative 31; Mismatches 80; Indels 33; Gaps 8;  
  
Qy 1 MKASLASLSAAYLLMTPTGKLTAKTNGSCVATNMQE--INQFSD---IRGSVOA 55  
Db 304 LPASLNDQLPGHTRVMTGSDSQK---ECVILKORPECWCSDSATDEQLFRCELSV 358  
Qy 56 KQGNIDIRLRRTESLDPTKPRANRCLRLHLRL-YLDRVFNQYQTPDHYT----- 105  
Db 359 EKSTVLOSELBESCKLOELFENKNCCLTITILMALDPLVYKKTLOQFSTLKAVDNR 418  
Qy 106 -----LRKISLANSFLTIK---KDLRLCHAHNTCHGSEAMKKYSQI-LSH--FEKL 152  
Db 419 AAYLDLRSKFLSNSVLMKEYADVRLAHKDLTVLCHLEQLLVTLHLSHRLBAL 478  
Qy 153 EPQAIVAKL 162  
Db 479 PPALALRCL 488  
  
RESULT 9  
S64594  
Probable beta-adaptin YK5 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein G9331; protein YGR261C  
C:Species: Saccharomyces cerevisiae  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004  
R:Armstrong, S.A.; Agostoni Carbone, M.L.; Melchiorreto, P.; Plevani, P.; Martegani, E.; Var  
submitted to the Protein Sequence Database, May 1996  
A:Accession: S64594  
A:Reference number: S64591  
A:Molecule type: DNA  
A:Residues: 1-809 <PAN>  
A:Cross-references: UNIPROT:P46682; EMBL:Z73046; NID:g1323474; PID:e243689; PID:g1323475  
A:Experimental source: strain S288C  
R:Robinson, L.C.; Engle, H.M.; Panek, H.R.  
submitted to the EMBL Data Library, September 1995  
A:Description: Suppressors of loss of yeast casein kinase 1 function define the four sub  
A:Reference number: S63439  
A:Accession: S63450  
A:Molecule type: DNA  
A:Residues: 1-26, 'PLSVNVP', '36-723', 'T', '725-795', '801-809 <ROB>  
A:Cross-references: EMBL:U35411; NID:g1017728; PID:g1017729  
C:Genetics:  
A:Gene: SGD:YK55  
A:Cross-references: SGD:S0003493; MTPS:YGR261C  
A:Map position: 7K  
  
Query Match 10.3%; Score 93.5; DB 2; Length 809;  
Best Local Similarity 24.1%; Pred. No. 0.65;  
Matches 48; Conservative 39; Mismatches 73; Indels 39; Gaps 10;  
  
Qy 2 KASSLASLSAAYLLMTPTGKLTAKTNGSCVATNMQEINQFSDIRGSVOADGND 61  
Db 21 EAAAVATSKLGSSTYY--SONINPOQLVTLINSNSREVADAMKRTISIASDDSD 78

Qy 62 IRI-----LRRTESLDPTKPRANRCLRLHLRLYLDRVFNQYQTPDHYTLRKISLANSFL 117  
Db 79 VQLFADYVKNITNDIK-----VKRLHLVLLRFEN---DPNLTLSLNSQKSL 128  
Qy 118 TIKDLRLCHAHNTCHGSEAMKKYSQIISHPEK--LEPOA-----AVTK--ALGE 164  
Db 129 DSNSELR-CFA--LSALSDMSSSLPIIHTVTKLVTPSAMVKGVALAIITLYRAGK 185  
Qy 165 -----IDLLOMMEETE 176  
Db 186 NDYHELDIDIKELMADTD 204  
  
RESULT 10  
F83128  
Probable transcription regulator PA4135 (imported) - Pseudomonas aeruginosa (strain PA01  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: F83128  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lam,  
, Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F83128  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140 <STO>  
A:Cross-references: UNIPROT:Q9HWP6; GB:AE004630; GB:AE004091; NID:G9950337; PIDN:AA0752  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4135  
  
Query Match 9.3%; Score 85; DB 2; Length 140;  
Best Local Similarity 24.5%; Pred. No. 0.55;  
Matches 25; Conservative 25; Mismatches 42; Indels 10; Gaps 3;  
  
Qy 62 IRIIRTSLODTPKPRANRCLRLHLRLYLDRVFNQYQTPDHYTLRKISLANS- 115  
Db 40 IRIIRQGESESYQLANQACTLRPMGTGLRLERDGVIRKMAKXOR-RYYVLTKEG 98  
Qy 116 ---FLTIRKDLRLCHAHNTCHGSEAMKKYSQIISHPEKLP 154  
Db 99 QQCFTVSGDMKKNYQRIQRRFGEKLAQLLELNEKLRP 140  
  
RESULT 11  
T33346  
Hypothetical protein C16A11.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T33346  
R:Johnson, D.; Biewald, T.  
submitted to the EMBL Data Library, July 1998  
A:Description: The sequence of C. elegans cosmid C16A11.  
A:Reference number: Z21328  
A:Accession: T33346  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-646 <JOH>  
A:Cross-references: UNIPROT:O76579; EMBL:AF077536; PIDN:AAC26261.1; GSPDB:GN00020; CESP:  
A:Experimental source: strain Bristol N2; clone C16A11  
C:Genetics:  
A:Gene: CESP:C16A11.5  
A:Map position: 2  
A:Introns: 35/3; 72/1; 94/3; 129/3; 184/3; 205/1; 279/3; 387/3; 505/2; 540/2; 570/3  
  
Query Match 9.0%; Score 81.5; DB 2; Length 646;  
Best Local Similarity 26.1%; Pred. No. 7.4;  
Matches 36; Conservative 22; Mismatches 49; Indels 31; Gaps 8;

Qy 29 NIGSCVIAITNIOEIRNGSDIRGSVQAKDNIDIRL-----RTESLODTKPARNC 80  
 Db 176 NQACAFVDRSLRQ-RNSNDHPIVQELDSMKSIETIQPIORAKKAVPIDEKRGSYC 234  
 Qy 81 CL-LHRLRLVLD-----RVFKNYQTPD--HYTLKRISLANSPLTIKDLRLCAHMTCC 132  
 Db 235 ILAVALFELFENIIGWSRVFEKHVPKIIEYVL-KIPL-----LIFKSELPPPHIKTA 288  
 Qy 133 HCGEEMAKKYSOILSHFE 150  
 Db 289 H-----LHRLLSFE 298

## RESULT 12

S46367  
 protein kinase CDC7 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 16-Aug-2004  
 C/Accession: S46367; T39888  
 R/Fankhauser, C.; Simanis, V.  
 EMBO J. 13, 3011-3019, 1994  
 A/Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation in  
 A/Reference number: S46367; PMID:94313982; PMID:8039497  
 A/Accession: S46367  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1062 <FAN>  
 A/Cross-references: UNIPROT:P41892; EMBL:X78799; NID:G521098; PIDN:CAA5382.1; PID:G5210  
 A/Experimental source: wildtype 972 h minus  
 A/Note: mRNA sequencing was also done to confirm the intron borders  
 R/Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, February 1999  
 A/Reference number: Z21860  
 A/Accession: T39888  
 A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-1062 <SAU>  
 A/Cross-references: EMBL:AL035537; PIDN:CA836886.1; GSPDB:GN00067; SPDB:SPBC21.06C  
 A/Experimental source: strain 972h-; cosmid c21  
 C/Genetics:  
 A/Gene: CDC7, SPDB:SPBC21.06C  
 A/Map position: II; 2  
 A/Intons: 9/3; 54/3; 64/3; 86/2; 171/1; 325/1; 405/3; 427/1; 544/3; 589/3  
 C/Function:  
 A/Description: essential for septum formation and cell division  
 C/Superfamily: protein kinase homology  
 C/Keywords: ATP; cell division; phosphotransferase; protein kinase  
 F/7-259/Domain: protein kinase homology <KIN>  
 F/15-23/Region: protein kinase ATP-binding motif

Query Match 8.8%; Score 81; DB 2; Length 1062;  
 Best Local Similarity 30.2%; Pred. No. 15;  
 Matches 32; Conservative 20; Mismatches 44; Indels 10; Gaps 4;

Qy 23 TGLKTLNIGSCVIAITNIOEIRNG-PSDIRGSVQAKDNIDIRLIRTESLODTKPARNC 81  
 Db 466 TGLCTLVANCKYSGMKNBENEDGESDIPDSIERENLENDIE-----NNIALDKRTILAS 520  
 Qy 82 LLRLRLVLDVRFKNTQTPDHYTLRKISLANSPLTIKDLRLCAHMTCC 127  
 Db 521 LLSLGLSLRD---KNIGSKD-TVDSQIASILSEDLISLKRRIIOAH 562

## RESULT 13

T19925  
 hypochlorite protein C44C10.4 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T19925  
 R/Cottage, A.  
 submitted to the EMBL Data Library, February 1996  
 A/Reference number: Z19197  
 A/Accession: T19925

A/Status: preliminary; translated from GB/EMBL/DBD  
 A/Molecule type: DNA  
 A/Residues: 1-542 <WIL>  
 A/Cross-references: UNIPROT:Q18616; EMBL:Z69787; PIDN:CAA93638.1; GSPDB:GN00028; CESP:C4  
 A/Experimental source: clone C44C10  
 C/Genetics:  
 A/Gene: CESP:C44C10.4  
 A/Map position: X  
 A/Intons: 66/3; 229/3; 309/1; 328/3; 398/3

Query Match 8.8%; Score 80; DB 2; Length 542;  
 Best Local Similarity 23.2%; Pred. No. 8.4;  
 Matches 29; Conservative 25; Mismatches 43; Indels 28; Gaps 4;

Qy 39 LOEIRNGSDIRGSVQAKDNIDIRLIRTESLODTKPARNCCLRLRLVLDVRFKNT 98  
 Db 212 IQETKEKVAEQLKVNANAKMPLISRYSEAIIPKQTPSPN-----FKKN 256  
 Qy 99 -----QTPDHY-----TLRKISLANSPLTIKDLRLCAHMTCHGGERAMKYSOI 145  
 Db 257 AIVRPKTHNHYDNLITVDKLSYLNKXTERRELLQFAVNHPPNNIRFSEBGPNIYARE 316  
 Qy 146 LSHFE 150  
 Db 317 IDYTE 321

## RESULT 14

AD1160  
 hypochlorite protein glp/glnQ (imported) - Agrobacterium tumefaciens (strain C58, Dupon  
 C/Species: Agrobacterium tumefaciens  
 C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C/Accession: AD1160  
 R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavyn, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ater, B.W.  
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A/Reference number: AB2577; PMID:21608550; PMID:11743193  
 A/Accession: AD1160  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-502 <KUR>  
 A/Cross-references: UNIPROT:Q9WMP4; GB:AE008687; PIDN:AAL45698.1; PID:GI7743426; GSPDB:  
 C/Experimental source: strain C58 (Dupont)  
 C/Genetics:  
 A/Gene: glp/glnQ  
 A/Genome: plasmid

Query Match 8.4%; Score 76.5; DB 2; Length 502;  
 Best Local Similarity 24.6%; Pred. No. 17;  
 Matches 42; Conservative 23; Mismatches 37; Indels 69; Gaps 10;

Qy 10 LLSAAYLLMT-PSGL-----KTLNIGS---CVIATNIOEIRNGSDIRGSVQAKDNIDIRLIRTESLODTKPARNC 55  
 Db 206 LLAGVRYLLVTVPLTHVVAIDRLIRIGKQRPVSIVTSGLEBV-----SELDGARASGVAP 261  
 Qy 56 KQDNIDIRLIRTESLODTKPARNC-----LLRLVLDVRFKNTQTPDHYTLRKISLANSPLTIK 86  
 Db 262 KGSGLDVRRLGMAVGDLDVKGVDLSVKPQSVTCIIIGPSGSGSTLRLGLNRLVVERKSGD 321  
 Qy 87 -----LRLVLDVRFKNTQTPDHYTLRKISLANSPLTIK 121  
 Db 322 ILIDGESILAMKRTILRRVGVVFGHPNLFPH-----TALENVWLSLKK 366

## RESULT 15

B90153  
 2-isopropylmalate synthase, probable (leuA-1) (imported) - Sulfolobus solfataricus  
 C/Species: Sulfolobus solfataricus  
 C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C:Accession: B90153

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: *Sulfolobus solfataricus* complete genome.

A:Reference number: A9139

A:Accession: B90153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-553 <KID>

A:Cross-references: UNIPROT:Q980Z1; GB:AB006641; NID:g13813259; PIDN:AAK40481.1; GSPDB:G

C:Genetics:

C:Gene: leuA-1

C:Superfamily: 2-Isopropylmalate synthase leuA

Query Match 8 4%; Score 76.5; DB 2; Length 553;

Best Local Similarity 19.6%; Pred. No. 19; Mismatches 61; Indels 65; Gaps 8;

Matches 39; Conservative 34; Mismatches 61; Indels 65; Gaps 8;

QY 24 GLKTLNLGSCVATWLOEIRNGFSDIRGSVGA---KDGNIID-----IRILRR 67

DB 232 GIHANNDIGCAVANSIMAIKAGARHVQGTINGIGERTGNADLIQIITLILKMGIALANG 291

QY 68 TESTIOTKPNRRC-----LRLRLRLYLDRVFKNYQTDPD----- 103

DB 292 QESLKLREVSRIYVEIIGLPENPYQPYGDNAFAHKAGVHVDAVMKVPRAVEHVDPSLV 351

QY 104 -----YTLRKISSLAN--SFL-----TIKXDLRLCHAHMTCHGEBAMKYSQILSHFE 150

DB 352 GNDKRFVISELSGTANLVSYLGIGIAVDKDERL-----KKALINKIKELERAGY 401

QY 151 KLE--POAAVVKALGELDI 167

DB 402 SFDVGPAASAILITLKEINI 420

Search completed: November 2, 2005, 18:48:01

Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 2, 2005, 18:40:05; Search time 177 Seconds

(without alignments)  
509.186 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 910  
Sequence: 1 MKASSLAFSLISAPFYLIWT.....AVKALGELDILLOMERTTE 176

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	906	99.6	176	1 IL20_HUMAN	Q9NYI1 homo sapien
2	672	73.8	176	1 IL20_MOUSE	Q9JXV9 mus musculu
3	337.5	37.1	177	1 IL19_HUMAN	Q9JHD0 homo sapien
4	281.5	30.9	176	2 O8CJ70	O8CJ70 mus musculu
5	266.5	29.3	175	2 Q7SK60	Q7SK60 tetraodon n
6	222	24.4	220	2 Q9Z5J3	Q9Z5J3 mus musculu
7	220	23.8	181	2 Q9Z5S4	Q9Z5S4 mus musculu
8	217	23.2	206	1 IL24_HUMAN	Q13007 homo sapien
9	191	21.0	183	1 MOB5_RAT	Q9J124 rattus norv
10	187	20.5	183	2 Q9WV8	Q9WV8 rattus norv
11	175.5	19.3	175	2 O6A2H4	O6A2H4 gallus gall
12	175.5	19.3	175	2 O6A2H5	O6A2H5 gallus gall
13	161.5	17.7	178	1 IL10_MACNE	P51497 macaca neme
14	161	17.7	177	2 Q8UZJ6	Q8UZJ6 cercopithec
15	157.5	17.3	178	1 IL10_MACFA	P51498 macaca fasc
16	157.5	17.3	178	1 IL10_MACMU	P51496 macaca mula
17	157.5	17.3	180	2 Q7T311	Q7T311 cypripus ca
18	156.5	17.2	150	2 Q7T311	Q7T311 homo sapien
19	156.5	17.2	178	1 IL10_FELCA	P55029 felis silve
20	156.5	17.2	178	1 IL10_HUMAN	P22301 homo sapien
21	155	17.0	170	1 BCRF_EBV	P03180 Epstein-Bar
22	155	17.0	170	2 Q777H2	Q777H2 human herpe
23	155	17.0	175	1 IL10_PIG	Q92905 sus scrofa
24	154.5	17.0	178	1 IL10_CERTE	P47965 meriones un
25	153	16.8	178	1 IL10_MERUN	P51746 cervus elap
26	151.5	16.6	179	1 IL10_CEREL	Q9T574
27	151	16.6	178	2 Q9T574	Q9T574 cyrtocolagus
28	147.5	16.2	178	1 Q9TVD3	Q9TVD3 equine herp
29	147.5	16.2	179	1 IL10_EH2	P18883 mus musculu
30	147	16.2	178	1 IL10_MOUSE	Q6FG69
31	145.5	16.0	178	2 Q6FG69	Q6FG69 homo sapien

32	144.5	15.9	160	2 Q923T1	Q923T1 sigmodon hi
33	144.5	15.9	174	1 IL10_TRIYU	Q97798 trichosturus
34	144.5	15.9	178	1 IL10_HORSE	Q28374 equus cabal
35	143.5	15.8	178	2 Q6VW71	Q6VW71 bubalus bub
36	143	15.7	171	2 Q9Q5L1	Q9Q5L1 herpessivus
37	142.5	15.7	178	1 IL10_BOVIN	P43480 bos taurus
38	142.5	15.7	178	2 Q8MK39	Q8MK39 salmistr sci
39	142	15.6	181	1 IL10_CANPA	P48411 canis famil
40	141.5	15.5	184	2 Q6L8N7	Q6L8N7 oncorhynch
41	140	15.4	178	2 Q665X4	Q665X4 lama glama
42	139.5	15.3	178	1 IL10_CANVO	Q921Y5 cavia porce
43	139	15.3	130	2 Q70327	Q70327 mesocricetu
44	138	15.2	178	1 IL10_RAT	P23456 rattus norv
45	136	14.9	185	2 Q6TV62	Q6TV62 bovine papu

## ALIGNMENTS

RESULT 1  
ID IL20\_HUMAN STANDARD; PRT; 176 AA.  
AC Q9NYI1; Q9EQ26;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10)  
DB (UNQ852/PRO1801).  
GN Name=IL20;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=2109717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8;  
RX Blumberg H., Conklin D., Xu W.F., Grossman A., Brender T.,  
RA Carollin S., Egan M., Foster D., Haldeman B.A., Haugen H.,  
RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,  
RA Prunkard D., Saxon S., Sprecher C., Wagie K., West J.,  
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;  
RT "Interleukin 20: discovery, receptor identification, and role in  
RT epidermal function.";  
RL Cell 104:9-19(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX Rieder M.J., Carrington D.P., Chung W.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RT "SeattleSNPs: NHRI HL66682 program for genomic applications, UW-  
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen Y., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schenfeld J.,  
RA Seshgiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [4]  
RP SEQUENCE OF 25-39.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";

```

RL Protein Sci. 13:2819-2824(2004).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC periclasia. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,
CC and other tissues.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF224267; AAF36679.1; -.
DR EMBL; AF402002; AAK84423.1; -.
DR EMBL; AY358320; AAO88686.1; -.
DR HSSP; Q9UHD0; IN1F.
DR Genem; HGNC:6002; IL20.
DR MIM; 605619; -.
DR GO; GO:0005576; E:extracellular; TAS.
DR GO; GO:0045517; F:interleukin-20 receptor binding; TAS.
DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. . .; TAS.
DR GO; GO:0045618; P:positive regulation of keratinocyte differ. . .; TAS.
DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. . .; TAS.
DR GO; GO:0050727; P:regulation of inflammatory response; TAS.
DR InterPro; IPR000098; Interleukin_10.
DR Prodom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR KW Cytokine; Direct protein sequencing; Signal.
FT CHAIN 1 24
FT SIGNAL 25 24 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
FT CONFLICT 48 48 E -> D (in Ref. 1).
FT CONFLICT 126 126 C -> S (in Ref. 3).
SQ SEQUENCE 176 AA; 20072 MW; 8385992500B6C447 CRC64;

Query Match 99.6%; Score 906; DB 1; Length 176;
Best Local Similarity 99.4%; Pred. No. 1.3e-80;
Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKASSLASLSAAYFLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIRDSVQAKDNI 60
DB 1 MKASSLASLSAAYFLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIRDSVQAKDNI 60
QY 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
DB 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
QY 121 KDLRLCHAMTCHGGEEMARKYQSILSHPEKLEPQAAVVKALGELDILLQMMEE 176
DB 121 KDLRLCHAMTCHGGEEMARKYQSILSHPEKLEPQAAVVKALGELDILLQMMEE 176

RESULT 2
IL19_MOUSE STANDARD; PRT; 176 AA.
ID IL19_MOUSE
AC Q9JUV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-20 precursor (IL-20) (four alpha helix cytokine ZCYTO10).
GN Name=IL20;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Skin;
RX MEDLINE=21097717; PubMed=1163236; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossman A., Bender T.,
RA Carrollo S., Sagan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,
RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Waggle K., West J.,
RA Whitmore T.E., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;
RA "Interleukin 20: discovery, receptor identification, and role in
RA epidermal function.";
RL Cell 104:9-19(2001).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC periclasia. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AF224267; AAF36680.1; -.
DR HSSP; Q9UHD0; IN1F.
DR MGD; MGI:1890473; IL20.
DR GO; GO:0045517; F:interleukin-20 receptor binding; IPI.
DR InterPro; IPR000079; 4_helix_cytokine.
DR Prodom; PD003687; Interleukin_10.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR KW Cytokine; Signal.
FT CHAIN 1 24
FT SIGNAL 25 24 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
SQ SEQUENCE 176 AA; 20097 MW; 08577AF656574771 CRC64;

Query Match 73.8%; Score 672; DB 1; Length 176;
Best Local Similarity 75.3%; Pred. No. 1.1e-57;
Matches 131; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

QY 1 MKASSLASLSAAYFLMTPTSTGLKTLNLGSCVATNLQETIRNGFSIRDSVQAKDNI 60
DB 1 MKGFLAFLGSAYGFLMTPLTGKTLHLGSCVITANLQAIQKFSIRDSVQAKDNI 60
QY 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
DB 61 DIRILRTTESLQDTKPARNCCLRLHLRLYLDRVFNKYQTPDHYTLRKISSLSANFLTIK 120
QY 121 KDLRLCHAMTCHGGEEMARKYQSILSHPEKLEPQAAVVKALGELDILLQMMEE 174
DB 121 KDLVCHSHMACHGGEEMARKYQILSHPELEPQAAVVKALGELGILLRWEE 174

RESULT 3
IL19_HUMAN STANDARD; PRT; 177 AA.
ID IL19_HUMAN
AC Q9UHD0; Q96OR4; Q9NUA0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Interleukin-19 precursor (IL-19) (Melanoma differentiation associated
DE protein-like protein) (NG.1).
GN Name=IL19; Synonyms=zMDA1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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CC MEDLINE=21040165; PubMed=11196675; DOI=10.1038/sj.gene.6363714;  
RA Gallagher G., Dickensheets H., Eskdale J., Izotova L.S.,  
RA Mitrochitschenko O.V., Peat J.D., Vasquez N., Peacka S., Donnelly R.P.,  
RA Kotonko S.V.;  
RT "Cloning, expression and initial characterization of interleukin-19  
RT (IL-19), a novel homolog of human interleukin-10 (IL-10).";  
RT Genes Immun. 1:442-450(2000).  
CC (2)  
CC SEQUENCE FROM N.A.  
RA Conklin D., Petersen J., Loften-Day C., Whitmore T., Muerer M.,  
RA Sexson S., Smith D., Lok S., Ponder T., O'Hara P.;  
RT "Homo sapiens homolog of melanoma differentiation associated gene";  
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
CC (3)  
CC SEQUENCE FROM N.A.  
RA Kotonko S.V., Peacka S.;  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC (4)  
CC SEQUENCE FROM N.A., AND VARIANT PHB-175.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peel C.L., Yi Q.,  
RA Nickerson D.A.;  
RT "SeattleSNPs: NHLBI HUG6682 program for genomic applications, UM-  
RT FRHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC (5)  
CC SEQUENCE OF 98-177 FROM N.A.  
RA Hall R.;  
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC (6)  
CC SEQUENCE OF 25-39.  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RT Protein Sci. 13:2819-2824(2004).  
CC (7)  
CC SUBCELLULAR LOCATION: Secreted.  
CC (8)  
CC (1- SIMILARITY: Belongs to the IL-10 family.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
CC  
CC EMBL; AF276915; AAC16755.1; -  
CC EMBL; AF192498; AAF06663.1; -  
CC EMBL; AY040367; AAK91776.1; ALT\_INIT.  
CC EMBL; AF390905; AAK64498.1; -  
CC EMBL; AL049615; CAB72342.1; -  
CC PDB; 1NIF; X-ray; A=19-177.  
CC Genew; HGNC:5990; IL19.  
CC MIM; 605687; -  
CC DR GO; GO:0005576; C:extracellular; NAS.  
CC DR GO; GO:0005125; F:cytokine activity; TAS.  
CC DR GO; GO:0006955; P:immune response; NAS.  
CC DR GO; GO:0007165; P:signal transduction; NAS.  
CC DR InterPro; IPR009079; 4\_helix\_cytokine.  
CC DR InterPro; IPR000098; Interleukin\_10.  
CC DR SMART; SM00188; Interleukin\_10.  
CC DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
CC DR 3D-structure; Cytokine; Direct protein sequencing; Glycoprotein;  
CC Polymorphism; Signal.  
CC FT SIGNAL 24  
CC FT CHAIN 25 177 Interleukin-19.  
CC FT CARBOHYD 56 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 135 N-linked (GlcNAc...) (Potential).  
CC FT VARIANT 175 S->F.  
CC FT SEQUENCE 177 AA; 20392 MW; 7CCFAC22177DB408 CRC64;  
SQ

Query Match

37.1%; Score 337.5; DB 1; Length 177;

Best Local Similarity 39.7%; Pred. No. 6, 7e-25;  
Matches 69; Conservative 36; Mismatches 64; Indels 5; Gaps 1;  
QY 1 MKASLSAFLSAAPAYLLMTPTSGTKTLNLSGCVATNIOBIRNGFSIRGSVOAKDGN 60  
DB 1 MLCQSVSLMLGTLITILCSVDNHGR-----RLISTDWHHEESFOEIKRAIOAADTTP 55  
QY 61 DIRLRRTESLQDTTPARCCILRLRLRYLDRVRKNVOTPPHYTLRKISLSANSFLYIK 120  
DB 56 NYTILSTLETTQIIPLDVCCVTKNLAPYRVRFVDFHDPKPKLIRKISLSANSFLYMQ 115  
QY 121 KOLRLCHAMTCHGCEAMKKYSQILSHPEKLEPQAAVVKALGELDILLQNMEE 174  
DB 116 KTLRQCEORQCHCRQEAATNATRVHDNYDQLEFVAAAKSKISGELDVFLAMINK 169

## RESULT 4

ID 08CJ70 PRELIMINARY; PRT; 176 AA.

AC 08CJ70;  
DT 01-MAR-2003 (TREMblrel. 23, Created)  
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Interleukin 19 (Fragment).  
GN Name=IL19;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss Webster/NIH;  
RX MEDLINE=22257669; PubMed=12370360;  
RY Liao Y.C., Liang W.G., Chen F.W., Hsu J.H., Yang J.J., Chang M.S.;  
RT "IL-19 induces production of IL-6 and TNF-alpha and results in cell  
RT apoptosis through TNF-alpha";  
RT J. Immunol. 169:4288-4297(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss Webster/NIH;  
RY Liao Y.-C., Chang M.-S.;  
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RX EMBL; AF453945; AAN40905.1; -  
DR HSSP; Q9UHD0; 1NIF.  
DR MGD; MGI:1890472; 1119.  
DR GO; GO:0006917; P:induction of apoptosis; IDA.  
DR GO; GO:0042326; P:interleukin-6 biosynthesis; IDA.  
DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IDA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000098; Interleukin\_10.  
DR ProDom; PD003687; Interleukin\_10; 1.  
DR SMART; SM00188; IL10; 1.  
FT NON TER 1  
SQ SEQUENCE 176 AA; 20287 MW; 73B6C1BC5407FDC CRC64;

Query Match 30.9%; Score 281.5; DB 2; Length 176;  
Best Local Similarity 38.6%; Pred. No. 2, 1e-19;  
Matches 56; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY 29 NLGSCVATNLOIRNGFSIRGSVOAKDGNIRIRLRRTESLQDTTPARCCILRLRL 88  
DB 24 SLRCLISVIMRLIESFHKIKAMQTKDFFKNTVL-SLENLRISFPGVCCNTNNLLT 82  
QY 89 LYLDVRVKNVOTPDHYTLRKISLSANSFLTIKDLRLCHAMTCHGCEAMKKYSQILSH 148  
DB 83 FYDVRVQDQHSLEVLARISSIANSLFVCQSLERCVHRCQNCQSEATNATRIHDN 142  
QY 149 FEKLEPQAAVVKALGELDILLQNMEE 173  
DB 143 YNQLSEVSSAALKSIGELNILLAWID 167

RESULT 5

Q7SK60  
ID Q7SK60 PRELIMINARY; PRT; 175 AA.  
AC Q7SK60;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Interleukin-20.  
GN Name=IL20;  
OS Tetradon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetradon.  
OX NCBI\_TaxId=99883;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed:12869211; DOI=10.1186/1471-2164-4-29;  
RA Lutfalla G., Croillius H.R., Strange-Thomann N., Jallion O.,  
Mogensen K., Monneron D.;  
RT "Comparative genomic analysis reveals independent expansion of a  
RT lineage-specific gene family in vertebrates: the class II cytokine  
RT receptors and their ligands in mammals and fish."  
RL BMC Genomics 4:29-29(2003).  
DR EMBL; AY294557; AAP57414.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005125; F:cytokine activity; IEA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000098; Interleukin\_10.  
DR ProDom; PD003687; Interleukin\_10; 1.  
DR SMART; SMO0188; IL10; 1.  
SQ SEQUENCE 175 AA; 19838 MW; D66FA67E0038E034 CRC64;

Query Match 29.3%; Score 266.5; DB 2; Length 175;  
Best Local Similarity 38.0%; Pred. No. 6e-18;  
Matches 57; Conservative 33; Mismatches 53; Indels 7; Gaps 3;

QY 26 KTLNLSGCVIATNLGIRNGFSDIRGSVOAKGNDIRLRTESLQTPKRNCCLRH 85  
DB 24 QTLNLSGCVIATNLGIRNGFSDIRGSVOAKGNDIRLRTESLQTPKRNCCLRH 82  
QY 86 LRLYLIDRVFKNYQTPDHYTLARKISLANSPLTI--KQDLRLCHAMTCHCGEAMKYS 143  
DB 83 VLQFIDKVFPSYLSHPNQGSSSLATFIITRKQIQGCH----CLGEGYQKQVD 138  
QY 144 QILSHPEKLEPOAAVYKALGELDILLQMMSE 173  
DB 139 SLIDAFNKLKASKAVLVKAVGELDTVLQWLO 168

RESULT 6  
ID Q925J3 PRELIMINARY; PRT; 220 AA.  
AC Q925J3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Th2-specific cytokine FISP.  
GN Name=IL24;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BALB/c;  
RX MEDLINE=21240641; PubMed=11342597;  
RA Schaefer G., Venkataraman C., Schindler U.,  
RT "FISP (IL-4-induced secreted protein), a novel cytokine-like molecule  
RT secreted by Th2 cells."  
RL J. Immunol. 166:5859-5863(2001).  
DR EMBL; AF333251; AAK52470.1; -;

DR MGD; MGI:2135548; IL24.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR ProDom; PD003687; Interleukin\_10; 1.  
DR SMART; SMO0188; IL10; 1.  
DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
SQ SEQUENCE 220 AA; 25168 MW; 5BF76C8612AC909D CRC64;  
Query Match 24.4%; Score 222; DB 2; Length 220;  
Best Local Similarity 34.4%; Pred. No. 1.8e-13;  
Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LLMTPSTGL--KTINLSSC-VIATNLGIRNGFSDIRGSVOAKGNDIRLRTESLQD 73  
DB 16 LLMNQVPLBQEFRRFGSCQVTGVLPDLMEAFWTKVQTQDDITSIRLL-KQVLRN 74  
QY 74 TKPANRCLLHLRLYLIDRVFKNYQTPDHYTLARKISLANSPLTIKQDLRLCHAMT 131  
DB 75 VSGASSCYLAHSLKFLYNTVFKYHSKIARFKVLRFSSTLANNTIVIMSQLOPSKNSM 134  
QY 132 CHCGEAMKYSQILSHPEKLEPOAAVYKALGELDILLQMMSE 174  
DB 135 LPIBSAHQRFLLFRFAFKQDLTEVALVKAGGEVDILLTMQK 177

RESULT 8  
ID IL24\_HUMAN STANDARD; PRT; 206 AA.  
AC Q13007; Q96DB0; Q96KG4;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)

Query Match 24.2%; Score 220; DB 2; Length 181;  
Best Local Similarity 34.4%; Pred. No. 2.3e-13;  
Matches 56; Conservative 30; Mismatches 71; Indels 6; Gaps 4;

QY 17 LLMTPSTGL--KTINLSSC-VIATNLGIRNGFSDIRGSVOAKGNDIRLRTESLQD 73  
DB 16 LLMNQVPLBQEFRRFGSCQVTGVLPDLMEAFWTKVQTQDDITSIRLL-KQVLRN 74  
QY 74 TKPANRCLLHLRLYLIDRVFKNYQTPDHYTLARKISLANSPLTIKQDLRLCHAMT 131  
DB 75 VSGASSCYLAHSLKFLYNTVFKYHSKIARFKVLRFSSTLANNTIVIMSQLOPSKNSM 134  
QY 132 CHCGEAMKYSQILSHPEKLEPOAAVYKALGELDILLQMMSE 174  
DB 135 LPIBSAHQRFLLFRFAFKQDLTEVALVKAGGEVDILLTMQK 177



```
DT 28-FEB-2003 (Rel. 41, last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
RT Cytokine-like protein Mob-5 precursor.
GN Name=Mob5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20387329; PubMed=10825166; DOI=10.1074/jbc.M001958200;
RT Zhang R., Tan Z., Liang P.;
RT "Identification of a novel ligand-receptor pair constitutively
RT activated by ras oncogenes."
RL J. Biol. Chem. 275:24436-24443(2000).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AF269251; AAF7553.1; -
DR Interpro; IPR009079; 4_helix_cytokine.
DR Interpro; IPR000098; Interleukin_10.
DR Prodom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 183 Cytokine-like protein Mob-5.
FT CAROXYD 76 76 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 183 AA; 21096 MW; AF7A11466C491AC4 CRC64;

Query Match
Best Local Similarity 33.1%; Score 191; DB 1; Length 183;
Matches 49; Conservative 31; Mismatches 60; Indels 8; Gaps 5;

QY 31 GSC-VIATNLQIRNGFSDIRGSVOAKDGNIDIRLRTESLDQTPANKRCCLRLHLRL 89
DB 34 GPCQVTGVLPBELWEAFVTWKVTKVQDELTSVRL-KQVLTQVSDAESCYLAHSLIKF 92
QY 90 YLDKVFKNYQTP--DHYTLRKISLSANGFLTIKKDLRLCHAMTCHGSEAMKXYSQILS 147
DB 93 YLNTVFKNYHSKIVKFKYKLSFSTLANNFLVIMSKLQPSKONAMLPISDSARRRFLLY 150
QY 148 H--PEKLEPOAAVVKALGELDILQWME 173
DB 151 HRTFKQLDIEVALAKAFGEVDILAMWQ 178

RESULT 10
Q9WVP8 PRELIMINARY; PRT; 183 AA.
AC Q9WVP8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE C49a.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=59308886; PubMed=10381256;
RX DOI=10.1002/(SICI)1097-4644(19990701)74:1<1::AID-JCB13-3.3.CO;2-D;
RX Soo C., Shaw W.W., Freymiller E., Longaker M.T., Bertolami C.N.,
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RA Chiu R., Tieu A., Ting K.;
RT "Cutaneous rat wounds express c49a, a novel gene with homology to the
RT human melanoma differentiation associated gene, mda-7."
RL J. Cell. Biochem. 74:1-10(1999).
DR EMBL; AF004774; AAB69171.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Interpro; IPR009079; 4_helix_cytokine.
DR Interpro; IPR000098; Interleukin_10.
DR Prodom; PD003687; Interleukin_10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
SQ SEQUENCE 183 AA; 21052 MW; FF69A96AFC473E4F CRC64;

Query Match
Best Local Similarity 32.2%; Score 187; DB 2; Length 183;
Matches 47; Conservative 29; Mismatches 66; Indels 4; Gaps 3;

QY 31 GSC-VIATNLQIRNGFSDIRGSVOAKDGNIDIRLRTESLDQTPANKRCCLRLHLRL 89
DB 34 GPCQVTGVLPBELWEAFVTWKVTKVQDELTSARLL-KPQVLTQVSDAESCYLAHSLIKF 92
QY 90 YLDKVFKNYQTP--DHYTLRKISLSANGFLTIKKDLRLCHAMTCHGSEAMKXYSQILS 147
DB 93 YLNTVFKNYHSKIVKFKYKLSFSTLANNFLVIMSKLQPSKONAMLPISDSARRRFLPHR 152
QY 148 HFEKLEPOAAVVKALGELDILQWME 173
DB 153 TFKQLDIEVALAKAFGEVDILAMWQ 178

RESULT 11
Q6A2H4 PRELIMINARY; PRT; 175 AA.
AC Q6A2H4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Interleukin-10.
GN Name=IL10;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OK NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Rotwell L., Young J., Zoorob R., Whitaker C.A., Hesketh P.,
RX Archer A., Smith A.L., Kaiser P.;
RT "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT Immune Response to Bimeria maxima."
RL J. Immunol. 173:2675-2682(2004).
DR EMBL; AJ621614; CAP21727.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; P:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Interpro; IPR009079; 4_helix_cytokine.
DR Interpro; IPR000098; Interleukin_10.
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR Prodom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
SQ SEQUENCE 175 AA; 20496 MW; A4966ABAADF8057 CRC64;

Query Match
Best Local Similarity 30.3%; Score 175.5; DB 2; Length 175;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

QY 1 MKASLAFSLAAVYLMTSTGKLTNLG-SCVIATNLQIRNGFSDIRGSVOAKDGN 59
DB 1 MOTCCQALLLLAACTL---PAHCLSEPTCLFSLPRLRLKRLKFKFEIKDYFSRDE 57
QY 60 IDIRLRTESLDQTPANKRCCLRLHLRLYLDRVFNKYQTPDHYTLRKISLSANGFLTI 119
```

```

Db      58 LNIQL-SELDLDFGFGCCSVSEMLFYTDEVLPRAMQSTSHQSGMDLGNLDEL 116
      120 KQDLRLCHAMTCHGCEAMKKYSQILSHPEKLEPOAAVVKALGELDILQNMEE 174
      117 KATIRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIVKAMGBDIFINYIEE 167

```

## RESULT 12

```

ID      06A2H5      PRELIMINARY;      PRT;      175 AA.
AC      06A2H5;
DT      25-OCT-2004 (TREMBLrel). 28, Created)
DT      25-OCT-2004 (TREMBLrel). 28, Last sequence update)
DE      Interleukin-10.
GN      Name=IL-10;
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]

```

```

RA      Rotherwell L., Young J., Zorob R., Whitaker C.A., Hesketh P.,
RA      Archer A., Smith A.L., Kaiser P.;
RT      "Cloning and Characterization of Chicken IL-10 and Its Role in the
RT      Immune Response to Elmeria maxima.";
RL      J. Immunol. 173:2675-2682 (2004).
DR      EMBL; AF621254; CAP18432.1; -.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0005125; P:cytokine activity; IEA.
DR      GO; GO:0006955; P:immune response; IEA.
DR      InterPro: IPR000979; 4 helix cytokine.
DR      InterPro: IPR000098; Interleukin_10.
DR      Pfam; PF00726; IL10; 1.
DR      PRINTS; PR01294; INTERLEUKIN10.
DR      ProDom; PD003687; Interleukin_10; 1.
DR      SMART; SM00188; IL10; 1.
SQ      SEQUENCE 175 AA; 20514 MW; B0966BEAPFB050 CRC64;

```

```

Query Match      19.3%; Score 175.5; DB 2; Length 175;
Best Local Similarity 30.3%; Pred. No. 5e-09;
Matches 53; Conservative 32; Mismatches 81; Indels 9; Gaps 5;

```

```

QY      1 MKASSLAFSLLSAFLMTSPGKLTNG-SCVATNLOIRNGPSDIRGSVOADGN 59
      1 MPTCCQALLLILACTL---PAHCLEPTCLHSELLPARLRKRVKFEIKDYFQSRDDE 57
      60 IDRIIRRTESLDTPKPRNCCLLRLRLYLDRVFKNYOTPDHYTLRKISLSANSEFLT 119
      58 LNIQL-SELDLDFGFGCCSVSEMLFYTDEVLPRAMQSTSHQSGMDLGNLDEL 116
      120 KQDLRLCHAMTCHGCEAMKKYSQILSHPEKLEPOAAVVKALGELDILQNMEE 174
      117 KATIRCHRFPTC---EKRSKAIKQIKETFEKMD-ENGIVKAMGBDIFINYIEE 167

```

## RESULT 13

```

ID      IL10_MACNE      STANDARD;      PRT;      178 AA.
AC      P51497;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory
DE      factor) (CSIF).
GN      Name=IL10;
OS      Macaca nemestrina (Pig-tailed macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9545;

```

```

      22 STGLKTLNIGSCV-----IATNLOIRNGPSDIRGSVOADGNIDRIIRRTESLDTPK 76
      19 SPQGTQSENSCTRFPGNLPMLRLDRDAFSAVKTFFQKMD-QLD-NILKESLDFPFK 76
      77 ANRCCLRLRLRLYLDRVFKNYOTPDHYTLRKISLSANSEFLTIKQDLRLCHAMTCHG 136
      77 YLGGQALSEMIQYLYEAVWQAEHNDPDIKEHVNLSIGENIKTLRLRLRCHRFPTC---E 133
      137 EAMKKYSQILSHPEKLEPOAAVVKALGELDILQNMEE 173
      134 NKSAVEQVWNAFSAKQ-EKGVYKAMSEDFIFINYIEE 169

```

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=PT 10000;
RX      MEDLINE=96003435; PubMed=7561102;
RA      Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT      "Comparative sequence analysis of cytokine genes from human and
RT      nonhuman primates.";
RL      J. Immunol. 155:3946-3954 (1995).
CC      -1- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC      including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC      activated macrophages and by helper T cells (By similarity).
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Belongs to the IL-10 family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      DR      HSSP; P22301; ILK3.
CC      DR      GO; GO:0005576; C:extracellular; ISS.
CC      DR      GO; GO:0005141; P:interleukin-10 receptor binding; ISS.
CC      DR      GO; GO:0006916; P:anti-apoptosis; ISS.
CC      DR      GO; GO:0030183; P:B-cell differentiation; ISS.
CC      DR      GO; GO:0042100; P:B-cell proliferation; ISS.
CC      DR      GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
CC      DR      GO; GO:0030097; P:hemopoiesis; ISS.
CC      DR      GO; GO:0006954; P:inflammatory response; ISS.
CC      DR      GO; GO:0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
CC      DR      GO; GO:0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
CC      DR      GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
CC      DR      GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
CC      DR      GO; GO:0045191; P:regulation of isotype switching; ISS.
CC      DR      GO; GO:0042092; P:T-helper 2 type immune response; ISS.
CC      DR      GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
CC      DR      InterPro: IPR000979; 4 helix cytokine.
CC      DR      InterPro: IPR000098; Interleukin_10.
CC      DR      Pfam; PF00726; IL10; 1.
CC      DR      PRINTS; PR01294; INTERLEUKIN10.
CC      DR      ProDom; PD003687; Interleukin_10; 1.
CC      DR      SMART; SM00188; IL10; 1.
CC      DR      PROSITE; PS00520; INTERLEUKIN_10; 1.
CC      CYTOKINE; Glycoprotein; Signal.
CC      FT      SIGNAL 1 18 Potential.
CC      FT      CHAIN 19 178 Interleukin-10.
CC      FT      DISULFID 30 126 By similarity.
CC      FT      DISULFID 80 132 By similarity.
CC      FT      CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
SQ      SEQUENCE 178 AA; 20560 MW; 35CC0D9D49E70718 CRC64;

```

```

Query Match      17.7%; Score 161.5; DB 1; Length 178;
Best Local Similarity 28.7%; Pred. No. 1.2e-07;
Matches 45; Conservative 31; Mismatches 70; Indels 11; Gaps 5;

```

```

QY      22 STGLKTLNIGSCV-----IATNLOIRNGPSDIRGSVOADGNIDRIIRRTESLDTPK 76
      19 SPQGTQSENSCTRFPGNLPMLRLDRDAFSAVKTFFQKMD-QLD-NILKESLDFPFK 76
      77 ANRCCLRLRLRLYLDRVFKNYOTPDHYTLRKISLSANSEFLTIKQDLRLCHAMTCHG 136
      77 YLGGQALSEMIQYLYEAVWQAEHNDPDIKEHVNLSIGENIKTLRLRLRCHRFPTC---E 133
      137 EAMKKYSQILSHPEKLEPOAAVVKALGELDILQNMEE 173
      134 NKSAVEQVWNAFSAKQ-EKGVYKAMSEDFIFINYIEE 169

```

## RESULT 14

Q8UJZ6		
ID	Q8UJZ6	PRELIMINARY; PRT; 177 AA.
AC	Q8UJZ6;	
DT	01-MAR-2002 (TrEMBLrel. 20, Created)	
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	BCRF1.	
OS	Cercopithecine herpesvirus 15 (Rhesus Epstein Barr virus).	
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	
OC	Gammaherpesvirinae; Lymphocryptovirus.	
OX	NClTaxID=45455;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=LCL8664;	
RX	MEDLINE=99412410; PubMed=10482645;	
RA	Rivailler P., Quink C., Wang F.;	
RT	"Strong selective pressure for evolution of an Epstein-Barr virus	
RT	LMP2B homolog in the rhesus lymphocryptovirus.";	
RL	J. Virol. 73:867-887(1999).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=LCL8664;	
RX	MEDLINE=97048062; PubMed=8892903;	
RA	Franken M., Devergne O., Rosenzweig M., Annie B., Kieff E., Wang F.;	
RT	"Comparative analysis identifies conserved tumor necrosis factor	
RT	receptor-associated factor 3 binding sites in the human and simian	
RT	Epstein-Barr virus oncogene LMP1.";	
RL	J. Virol. 70:7819-7826(1996).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=LCL8664;	
RX	MEDLINE=20304984; PubMed=10846073;	
RA	DOI=10.1128/JVI.74.13.5921-5932.2000;	
RT	Jiang H., Cho Y.G., Wang F.;	
RT	"Structural, functional, and genetic comparisons of Epstein-Barr virus	
RT	nuclear antigen 3A, 3B, and 3C homologues encoded by the rhesus	
RT	lymphocryptovirus.";	
RL	J. Virol. 74:5921-5932(2000).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=LCL8664;	
RX	MEDLINE=20440633; PubMed=10970361;	
RA	Rea P., Jiang H., Wang F.;	
RT	"Cloning of the rhesus lymphocryptovirus viral capsid antigen and	
RT	Epstein-Barr virus-encoded small RNA homologues and use in diagnosis	
RT	of acute and persistent infections.";	
RL	J. Clin. Microbiol. 38:3219-3225(2000).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=LCL8664;	
RA	MEDLINE=21602573; PubMed=1179708; DOI=10.1128/JVI.76.1.421-426.2002;	
RT	Rivailler P., Jiang H., Cho Y.G., Quink C., Wang F.;	
RT	"Complete nucleotide sequence of the rhesus lymphocryptovirus: genetic	
RT	validation for an Epstein-Barr virus animal model.";	
RL	J. Virol. 76:421-426(2002).	
DR	EMBL; AY037858; AAK95412.1; --	
DR	HSSP; P22301.1INR.	
DR	GO; GO:0005516; C:extracellular; IEA.	
DR	GO; GO:0005125; F:Cytokine activity; IEA.	
DR	GO; GO:0006955; P:immune response; IEA.	
DR	Pfam; PF00726; IL10; 1.	
DR	PRINTS; PR01294; INTRLEUKIN10.	
DR	ProDom; PD003687; interleukin_10; 1.	
DR	SMART; SMO0188; IL10; 1.	
DR	PROSITE; PS00520; INTERLEUKIN_10; 1.	
DR	SEQUENCE 177 AA; 20545 MW; 5F94050532E63A36 CRC64;	

```

DB      40  LRDRARFASRKTFQPKD-QLD-NILKKSLEDFPGVIGQCALSMIOFYILEBWRQA  97
QY      99  QTPDHVTLRKISSIANSFLTIKQDLRIAHMTCHGEEAMKRYQSILSFPEKLEPOAAV  158
DB      98  ENQDPHAKENHVNISGENMLKTLRLRLRCHRFLLPC---ENKSKAVEGQVNAFSLQ-EGKV  153
QY      159 VKALGEDLIILQWME 173
DB      154 YKAMSEFDIFLTYLTS 168

RESULT 15
IL10_MACPA
ID      IL10_MACPA  STANDARD;  PRT;  178 AA.
AC      P79938;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory
DE      factor) (CSIF).
GN      Name=IL10;
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cerepitheidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tatemul M.;
RL      Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Inhibits the synthesis of a number of cytokines,
CC      including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by
CC      activated macrophages and by helper T cells (By similarity).
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- SIMILARITY: Belongs to the IL-10 family.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL, AB000514; BAA19132.1; -.
DR      HSSP; P22301; 1LK3.
DR      GO; GO:0005576; C:extracellular; ISS.
DR      GO; GO:0005141; F:interleukin-10 receptor binding; ISS.
DR      GO; GO:0006916; P:anti-apoptosis; ISS.
DR      GO; GO:0030183; P:B-cell differentiation; ISS.
DR      GO; GO:0042100; P:B-cell proliferation; ISS.
DR      GO; GO:0007253; P:cytoplasmic sequestering of NF-kappaB; ISS.
DR      GO; GO:0030091; P:hemopoiesis; ISS.
DR      GO; GO:0006954; P:inflammatory response; ISS.
DR      GO; GO:0045077; P:negative regulation of interferon-gamma bio. . .; ISS.
DR      GO; GO:0045347; P:negative regulation of MHC class II biosynt. . .; ISS.
DR      GO; GO:0045019; P:negative regulation of nitric oxide biosynt. . .; ISS.
DR      GO; GO:0042130; P:negative regulation of T-cell proliferation; ISS.
DR      GO; GO:0045192; P:regulation of isotype switching; ISS.
DR      GO; GO:0007260; P:T-helper 2 type immune response; ISS.
DR      GO; GO:0007260; P:tyrosine phosphorylation of STAT protein; ISS.
DR      InterPro; IPR000979; 4 helix cytokine.
DR      InterPro; IPR000098; Interleukin_10.
DR      Pfam; PF00726; IL10; 1.
DR      PRINTS; PR01294; INTRLEUKIN10.
DR      ProDom; PD003687; Interleukin_10; 1.
DR      SMART; SM00188; IL10; 1.
DR      PROSITE; PS00520; INTERLEUKIN_10; 1.
KW      Cytokine; Glycoprotein; Signal.
FT      SIGNAL 1 18 Potential.
FT      CHAIN 19 178 Interleukin-10.
FT      DISULFD 30 126 By similarity.

```



FT	DISULFID	80	132	By similarity.
FT	CARBOHYD	134	134	N-linked (GlcNAc... ) (Potential)..
SQ	SEQUENCE	178 AA;	20585 MW;	35CEDD98B3B8A718 CRC64;

Query Match	17.3%	Score 157.5	DB 1	Length 178
Best Local Similarity	28.7%	Pred. No. 2.9e-07		
Matches 45, Conservative	30, Mismatches 71,			Indels 11, Gaps 5,

```

Qy 22 STGLKTLNLGSCV-----IATNLQEIIRNGFSFDIRGSVAKDGNIDIRILARTESLDOTKP 76
      | | : | | : | | : | | : | | : | |
Db 19 SPGGQTGSNSCTRFPGNLPMLRLDLRAFAFSRVKTFPQMKD-QLD-NILKESLLEDFEK 76

```

Qy 77 ANRCCLRLHLRLYLDRVFKNYQTPHYTLRKISLANSPLTIKODLRLLCHAMTCHGE 136  
:::|::|::|:  
Db 77 YLGCAALSEMTGYLEEVMPQAEHHDPDIKEHVNSLGLENLKTLRLRLRGRHFPC---E 133

Qy 137 EAMKYSQILSHFEKLEPQAAVVKALGELDILOQME 173  
134 NKSKAVEQVKNAFSKLQ-EKGVYKAMSEFDIFINITYE 169

Search completed: November 2, 2005, 18:51:05  
job time : 180 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 2, 2005, 18:48:07 ; Search time 176 Seconds  
(without alignments)

512.079 Million cell updates/sec

Title: US-10-748-484-2

Perfect score: 176  
Sequence: 1 MKASSLAFSLSAFYLLMT.....AVVKALGLDILLQMEETE 176

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4229

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	128	72.7	176	1	IL20_HUMAN	Q9NYI1 homo sapien
2	13	7.4	176	1	IL20_MOUSE	Q9JXV9 mus musculi
3	8	4.5	137	2	IL2K4	O612K4 picophilus
4	8	4.5	249	1	SURE_PSEPK	O88M11 pseudomonas
5	8	4.5	279	2	O9KDB7	O9KDB7 bacillus ha
6	8	4.5	305	2	O8UIB8	O8UIB8 agrobacteri
7	8	4.5	396	2	O82S35	O82S35 nitrosomona
8	8	4.5	489	1	ANSP_STRCO	O9X7P0 streptomyce
9	8	4.5	517	1	MURE_BIFLO	O8G4M3 bifidobacte
10	8	4.5	531	2	O7ZVGO	O7ZVGO brachydanio
11	8	4.5	698	2	O83BA7	O83BA7 coxiella bu
12	8	4.5	717	1	P5CS_LYCES	O96480 l delta 1-p
13	8	4.5	719	2	O7MBR3	O7MBR3 vibrio vuln
14	8	4.5	725	2	O8E874	O8E874 shewanella
15	8	4.5	762	2	O9XGC4	O9XGC4 vitis vinif
16	8	4.5	1277	2	O6SLR3	O6SLR3 cochlidiolu
17	8	4.5	1908	2	O8ASB3	O8ASB3 bacteroides
18	8	4.0	69	2	O8ITP9	O8ITP9 methanosarc
19	8	4.0	90	2	O8NTP1	O8NTP1 corynebacte
20	8	4.0	91	2	O8UUS4	O8UUS4 gallus galli
21	8	4.0	94	2	O8UUG7	O8UUG7 gallus galli
22	8	4.0	96	2	O8CES3	O8CES3 mus musculi
23	8	4.0	97	2	O76Z23	O76Z23 bacterioph
24	8	4.0	97	2	O8R9M3	O8R9M3 thermosane
25	8	4.0	98	2	O6ITW6	O6ITW6 cordylus wa
26	8	4.0	107	2	O846H4	O846H4 uncultured
27	8	4.0	122	2	O6MAG4	O6MAG4 paracitlami
28	8	4.0	122	2	O6IUM3	O6IUM3 human immun
29	8	4.0	125	2	O7RWX0	O7RWX0 neurospora
30	8	4.0	131	2	O9RLP5	O9RLP5 planktochri
31	8	4.0	138	2	O9K4X8	O9K4X8 planktochri

32	7	4.0	141	2	O8MPC9	O8MPC9 taenia soli
33	7	4.0	145	2	O88188	O88188 san miguel
34	7	4.0	152	2	O74J72	O74J72 lactobacill
35	7	4.0	156	2	O6TV02	O6TV02 yaba monkey
36	7	4.0	167	2	O8GBW7	O8GBW7 planktochri
37	7	4.0	172	2	O9R385	O9R385 planktochri
38	7	4.0	172	2	O9RLF3	O9RLF3 planktochri
39	7	4.0	172	2	O9RLP6	O9RLP6 planktochri
40	7	4.0	183	2	O65XE9	O65XE9 oryza sativ
41	7	4.0	184	2	O680Y9	O680Y9 arabidopsis
42	7	4.0	194	2	O6DC06	O6DC06 brachydanio
43	7	4.0	195	2	O9DB50	O9DB50 lotus japon
44	7	4.0	196	1	RAC2_LOTJA	O6V0U7 xanthomona
45	7	4.0	197	2	O6V0U7	O6V0U7 streptomyce
46	7	4.0	201	2	O07640	O07640 caenorhabdi
47	7	4.0	208	2	O17158	O17158 caenorhabdi
48	7	4.0	210	2	O9K4W9	O9K4W9 oscillator
49	7	4.0	213	2	O9S1Y7	O9S1Y7 arabidopsis
50	7	4.0	217	2	O91ZY6	O91ZY6 rattus norv
51	7	4.0	217	2	O35047	O35047 mus musculi
52	7	4.0	218	2	O6S109	O6S109 paenibacill
53	7	4.0	224	1	G1DB_MYCTU	O53597 mycobacteri
54	7	4.0	235	2	O6H5U4	O6H5U4 oryza sativ
55	7	4.0	236	2	O6DVL7	O6DVL7 thermobia d
56	7	4.0	236	2	O9K4X7	O9K4X7 planktochri
57	7	4.0	240	2	O8GBV7	O8GBV7 oscillator
58	7	4.0	241	2	O9RSX2	O9RSX2 deinococcus
59	7	4.0	242	2	O63IM0	O63IM0 burkholderi
60	7	4.0	242	2	O63IM3	O63IM3 burkholderi
61	7	4.0	244	2	O9TIX9	O9TIX9 cyanidolum c
62	7	4.0	244	2	O882J9	O882J9 pseudomonas
63	7	4.0	245	2	O9K4X2	O9K4X2 oscillator
64	7	4.0	245	2	O9K4X4	O9K4X4 oscillator
65	7	4.0	251	2	O22186	O22186 caenorhabdi
66	7	4.0	262	2	O6DVL4	O6DVL4 thermobia d
67	7	4.0	263	2	O71U37	O71U37 gallus galli
68	7	4.0	282	2	O7U7E8	O7U7E8 synchococc
69	7	4.0	285	2	O6DJP2	O6DJP2 xenopus lae
70	7	4.0	286	2	O8KXA7	O8KXA7 chlorobium
71	7	4.0	289	2	O92QW7	O92QW7 rhizobium m
72	7	4.0	291	2	O8TRQ7	O8TRQ7 methanosarc
73	7	4.0	293	2	O9ZCP1	O9ZCP1 rickettsia
74	7	4.0	298	2	O88AJ4	O88AJ4 pseudomonas
75	7	4.0	304	2	O8IFLO	O8IFLO plasmodium
76	7	4.0	308	2	O94A06	O94A06 arabidopsis
77	7	4.0	308	2	O6DJA5	O6DJA5 xenopus tto
78	7	4.0	310	2	O87KJ6	O87KJ6 vibrio para
79	7	4.0	318	2	O6GLN0	O6GLN0 xenopus lae
80	7	4.0	321	2	O81V85	O81V85 bacillus an
81	7	4.0	321	2	O881C8	O881C8 pseudomonas
82	7	4.0	327	2	O67164	O67164 aquilex aeo
83	7	4.0	327	2	O83BW7	O83BW7 coxiella bu
84	7	4.0	332	2	O8P2B7	O8P2B7 streptococc
85	7	4.0	333	2	O66MH6	O66MH6 lycopersico
86	7	4.0	335	2	O6CTU9	O6CTU9 kluyveromyc
87	7	4.0	344	2	O6CTU9	O6CTU9 streptococc
88	7	4.0	345	2	O9A1A0	O9A1A0 arabidopsis
89	7	4.0	346	2	O38943	O38943 arabidopsis
90	7	4.0	354	2	O04440	O04440 oryza sativ
91	7	4.0	367	2	O751E0	O751E0 pyrococcus
92	7	4.0	368	2	O8U2K8	O8U2K8 allomyces m
93	7	4.0	382	2	O37395	O37395 lacticbactill
94	7	4.0	389	1	GALI_LACHE	O00052 lacticbactill
95	7	4.0	389	2	O74K94	O39688 daucus caro
96	7	4.0	391	2	O81CD6	O44X94 lacticbactill
97	7	4.0	392	2	O6NCT8	O81CD6 bacilllobac
98	7	4.0	398	2	O6XOG9	O6XOG9 rhodospseudo
99	7	4.0	411	2	O9BT50	O6XOG9 sus scrofa
100	7	4.0	411	2	O9BT50	O9BT50 homo sapien
101	7	4.0	413	2	O8EFQ2	O8EFQ2 shewanella
102	7	4.0	414	2	O6BZX3	O6BZX3 yarrowia li
103	7	4.0	419	2	O72Q94	O72Q94 leptospira
104	7	4.0	423	2	O72NS0	O72NS0 leptospira

105	7	4.0	423	2	08F7S1	08F7S1 leptoepira	178	7	4.0	749	2	0825G4	0825G4 streptomyc
106	7	4.0	423	2	08FA80	08FA80 escherichia	179	7	4.0	750	2	07S6E7	07S6E7 neuropep
107	7	4.0	426	2	031471	031471 bacillus eu	180	7	4.0	751	2	060934	060934 homo sapien
108	7	4.0	433	2	08F5W4	08F5W4 leptoepira	181	7	4.0	754	2	07LDM2	07LDM2 homo sapien
109	7	4.0	438	2	08FJ14	08FJ14 candida gla	182	7	4.0	754	2	084LH7	084LH7 oryza sativ
110	7	4.0	438	2	08W4W3	08W4W3 zea mays (m	183	7	4.0	761	2	082634	082634 arabidopsis
111	7	4.0	440	2	06A9Q3	06A9Q3 propionibac	184	7	4.0	762	1	MUS2_HELPJ	092114 helicobacte
112	7	4.0	441	2	084706	084706 chlamydia t	185	7	4.0	784	2	0881N5	0881N5 pseudomonas
113	7	4.0	444	2	09M8N1	09M8N1 arabidopsis	186	7	4.0	787	2	061B87	061B87 oligotroph
114	7	4.0	445	2	09SRX8	09SRX8 arabidopsis	187	7	4.0	835	1	STFB_CORNF	081TP0 corynabacte
115	7	4.0	445	2	06A177	06A177 desulfotale	188	7	4.0	850	2	09SR05	09SR05 arabidopsis
116	7	4.0	451	2	09W1F6	09W1F6 dirosophila	189	7	4.0	852	2	09P240	09P240 homo sapien
117	7	4.0	451	2	08R1T1	08R1T1 mus musculu	190	7	4.0	883	2	07SFP1	07SFP1 aethya gos
118	7	4.0	452	2	08BDM1	08BDM1 homo sapien	191	7	4.0	898	2	06K9J3	06K9J3 oryza sativ
119	7	4.0	453	2	08MUX9	08MUX9 homo sapien	192	7	4.0	915	2	09S7Y7	09S7Y7 arabidopsis
120	7	4.0	454	2	06CTI3	06CTI3 kluyveromyc	193	7	4.0	921	2	074XT3	074XT3 yersinia pe
121	7	4.0	456	2	0972Q9	0972Q9 sulfolobus	194	7	4.0	930	2	08ZBM7	08ZBM7 yersinia pe
122	7	4.0	456	2	06KRW4	06KRW4 bacillus an	195	7	4.0	931	2	07NBNO	07NBNO mycoplasma
123	7	4.0	463	2	06JBM3	06JBM3 bacillus ce	196	7	4.0	933	2	08D1A1	08D1A1 yersinia pe
124	7	4.0	463	2	081U49	081U49 bacillus an	197	7	4.0	968	2	091NJO	091NJO kadiptero vi
125	7	4.0	463	2	06HMC4	06HMC4 bacillus th	198	7	4.0	978	2	P91777	P91777 pacifastacu
126	7	4.0	469	2	06TQ31	06TQ31 homo sapien	199	7	4.0	979	2	081YES	081YES homo sapien
127	7	4.0	471	2	Q17960	Q17960 caenorhabdi	200	7	4.0	994	2	07QJ33	07QJ33 homo sapien
128	7	4.0	471	2	08GMB5	08GMB5 arabidopsis	201	7	4.0	1008	2	09H2U1	09H2U1 homo sapien
129	7	4.0	473	2	094606	094606 s jmc doma	202	7	4.0	1017	2	091KV5	091KV5 arabidopsis
130	7	4.0	475	2	06YZC9	06YZC9 oryza sativ	203	7	4.0	1018	2	06SHL7	06SHL7 uncultured
131	7	4.0	478	2	092UL2	092UL2 rhizobium m	204	7	4.0	1063	2	06MMJ3	06MMJ3 neuropep
132	7	4.0	480	2	048705	048705 arabidopsis	205	7	4.0	1100	2	09M319	09M319 arabidopsis
133	7	4.0	491	2	09VXK6	09VXK6 dirosophila	206	7	4.0	1101	2	Q7UV84	Q7UV84 rhodospirell
134	7	4.0	498	2	06BPPX9	06BPPX9 debaryomyc	207	7	4.0	1116	2	Q7RA41	Q7RA41 plasmodium
135	7	4.0	499	2	06S049	06S049 morus alba	208	7	4.0	1121	2	0942F3	0942F3 oryza sativ
136	7	4.0	499	2	087275	087275 pseudomonas	209	7	4.0	1138	2	08RXB5	08RXB5 arabidopsis
137	7	4.0	505	2	08S5V4	08S5V4 elaeagnus u	210	7	4.0	1140	2	06BRB6	06BRB6 debaryomyc
138	7	4.0	512	2	09KMC6	09KMC6 vibrio chol	211	7	4.0	1153	2	06B1P2	06B1P2 debaryomyc
139	7	4.0	514	2	06VZ29	06VZ29 canarypox v	212	7	4.0	1166	2	Q7Q992	Q7Q992 anopheles g
140	7	4.0	516	2	06CED6	06CED6 yarrowia li	213	7	4.0	1213	2	08ZKX1	08ZKX1 salmoneila
141	7	4.0	523	2	Q74HN4	Q74HN4 lactobacilli	214	7	4.0	1264	2	Q91SH3	Q91SH3 arabidopsis
142	7	4.0	532	2	08QU03	08QU03 nipah virus	215	7	4.0	1406	2	07TIC9	07TIC9 brachydanio
143	7	4.0	532	2	091K92	091K92 nipah virus	216	7	4.0	1556	1	PROS_DROVI	09U6A1 dirosophila
144	7	4.0	542	2	Q7YXQ3	Q7YXQ3 bordetella	217	7	4.0	1656	2	Q9XJ78	Q9XJ78 streptococc
145	7	4.0	542	2	Q7W647	Q7W647 bordetella	218	7	4.0	1938	2	06S0D5	06S0D5 bacteroides
146	7	4.0	547	1	NRM1_CINPA	NRM1_CINPA	219	7	4.0	1980	2	Q9VHD1	Q9VHD1 dirosophila
147	7	4.0	547	1	NRM1_BISBI	NRM1_BISBI	220	7	4.0	2144	2	084MP1	084MP1 oryza sativ
148	7	4.0	548	1	NRM1_BOVIN	NRM1_BOVIN	221	7	4.0	2165	2	Q13971	Q13971 caenorhabdi
149	7	4.0	548	1	NRM1_BOVIN	NRM1_BOVIN	222	7	4.0	3051	2	Q733Y78	Q733Y78 mycobacteri
150	7	4.0	548	1	NRM1_CEREL	NRM1_CEREL	223	7	4.0	3262	2	Q13788	Q13788 homo sapien
151	7	4.0	548	1	NRM1_CEREL	NRM1_CEREL	224	7	4.0	4563	1	APB_HUMAN	P04114 homo sapien
152	7	4.0	548	1	NRM1_SHEEP	NRM1_SHEEP	225	7	4.0	4563	1	Q72600	Q72600 homo sapien
153	7	4.0	554	2	Q9SFI2	Q9SFI2 arabidopsis	226	7	4.0	5216	2	Q9VXZ5	Q9VXZ5 dirosophila
154	7	4.0	555	1	NRM1_CHICK	NRM1_CHICK	227	7	4.0	5233	2	Q9NB71	Q9NB71 dirosophila
155	7	4.0	566	2	08MS58	08MS58 dirosophila	228	7	4.0	5237	2	Q9GR20	Q9GR20 nematostell
156	7	4.0	588	2	Q8PBK0	Q8PBK0 xanthomonas	229	7	3.4	37	2	Q7RZ29	Q7RZ29 neuropep
157	7	4.0	599	2	Q8KWP2	Q8KWP2 raietonia s	230	7	3.4	38	2	Q55471	Q55471 human immun
158	7	4.0	605	1	G6P1_LEIME	G6P1_LEIME	231	7	3.4	39	2	08K4D9	08K4D9 mus musculu
159	7	4.0	612	2	Q9F7N4	Q9F7N4 gamma-prote	232	7	3.4	40	2	08KXN3	08KXN3 chlorobium
160	7	4.0	624	1	AMYG_ARKAD	AMYG_ARKAD gamma-aden	233	7	3.4	50	2	08GXN8	08GXN8 arabidopsis
161	7	4.0	628	1	YE1F_SCHPO	YE1F_SCHPO schizosacch	234	7	3.4	53	2	08LWY0	08LWY0 laminaria d
162	7	4.0	628	2	Q8XIX6	Q8XIX6 clostridium	235	7	3.4	53	2	Q8SFF7	Q8SFF7 technetina
163	7	4.0	629	2	Q8BQSO	Q8BQSO pseudomonas	236	7	3.4	54	1	IOVO_LARRI	IOVO_LARRI latus rldid
164	7	4.0	639	2	Q6ZA03	Q6ZA03 oryza sativ	237	7	3.4	55	2	Q8VY72	Q8VY72 anabaena sp
165	7	4.0	649	1	VATI_CHLMU	VATI_CHLMU chlamydia m	238	7	3.4	56	1	YISI_BACSU	YISI_BACSU bacillus su
166	7	4.0	672	2	Q63HR6	Q63HR6 homo sapien	239	7	3.4	58	2	Q7P5D5	Q7P5D5 fusobacteri
167	7	4.0	686	2	Q8A4X3	Q8A4X3 bacteroides	240	7	3.4	58	2	Q8RHV3	Q8RHV3 yersinia pe
168	7	4.0	705	2	Q731Z4	Q731Z4 treponema d	241	7	3.4	59	2	Q69MW2	Q69MW2 oryza sativ
169	7	4.0	711	1	CG10_ARANTH	CG10_ARANTH arabidopsis	242	7	3.4	60	2	Q81ET6	Q81ET6 bacillus ce
170	7	4.0	711	1	Q6TFN3	Q6TFN3 bos taurus	243	7	3.4	61	2	Q7M7H6	Q7M7H6 vibrio vuln
171	7	4.0	726	2	Q823M0	Q823M0 chlamydomophi	244	7	3.4	61	2	Q7MKN0	Q7MKN0 vibrio vuln
172	7	4.0	726	2	Q88HM4	Q88HM4 pseudomonas	245	7	3.4	62	2	Q9X369	Q9X369 bacillus an
173	7	4.0	732	2	Q6CAM6	Q6CAM6 yarrowia li	246	7	3.4	62	2	Q90ZJ7	Q90ZJ7 anguilla an
174	7	4.0	740	2	Q9KJDT	Q9KJDT streptomyc	247	7	3.4	62	2	Q9DDE5	Q9DDE5 scophthalmu
175	7	4.0	743	2	Q9VWG6	Q9VWG6 dirosophila	248	7	3.4	63	1	V7K_BYDVP	V7K_BYDVP barley yell
176	7	4.0	744	2	Q92R95	Q92R95 rhizobium m	249	7	3.4	63	2	Q6BDU0	Q6BDU0 debaryomyc
177	7	4.0	744	2	Q92R95	Q92R95 rhizobium m	250	7	3.4	63	2	Q6BDU0	Q6BDU0 debaryomyc

251	6	3.4	63	2	Q7VP05	Q7VP05 chlamydia p	324	6	3.4	91	2	08G57	08G57 gallus galli
252	6	3.4	65	2	Q8E1T5	Q8E1T5 escherichia p	325	6	3.4	92	1	VER_HPV27	P36825 human papill
253	6	3.4	65	2	Q8K4H2	Q8K4H2 mus musculus	326	6	3.4	92	2	Q6A20	Q6A20 canis famli
254	6	3.4	66	2	Q9YCD4	Q9YCD4 aeropyrum p	327	6	3.4	92	2	Q7YAL5	Q7YAL5 fejevarya
255	6	3.4	66	2	Q7LH80	Q7LH80 saccharomyc	328	6	3.4	92	2	Q7LIU7	Q7LIU7 lactobacilli
256	6	3.4	66	2	Q6B8M1	Q6B8M1 gracillaria	329	6	3.4	94	2	Q94YM4	Q94YM4 rana nigrom
257	6	3.4	68	2	Q6S022	Q6S022 aleutian m	330	6	3.4	95	1	BCP4_RAB1T	Q02247 oryctolagus
258	6	3.4	69	2	Q97UN9	Q97UN9 sulfolobus	331	6	3.4	95	2	Q7Y3G5	Q7Y3G5 enterobacte
259	6	3.4	70	2	Q57TB9	Q57TB9 geobacillus	332	6	3.4	95	2	Q9ZB99	Q9ZB99 rhodococcus
260	6	3.4	70	2	Q8Z1B3	Q8Z1B3 salmonella	333	6	3.4	96	2	Q46626	Q46626 bos taurus
261	6	3.4	70	2	Q73115	Q73115 wolbachia p	334	6	3.4	97	2	Q7PA39	Q7PA39 rickettsia
262	6	3.4	71	1	Y698_ARCFU	Y698_ARCFU archaeoglob	335	6	3.4	97	2	Q7N3K9	Q7N3K9 photosynabu
263	6	3.4	71	1	YDGT_ECO57	YDGT_ECO57 escherichia	336	6	3.4	98	2	Q644M1	Q644M1 aneides har
264	6	3.4	71	1	YDGT_ECOL6	P64468 escherichia	337	6	3.4	98	2	Q9T286	Q9T286 caenorhabdi
265	6	3.4	71	1	YDGT_ECOLI	P64467 escherichia	338	6	3.4	100	2	Q7R8G4	Q7R8G4 plasmodium
266	6	3.4	71	1	YDGT_SHIFL	P64470 shigella fl	339	6	3.4	100	2	Q82165	Q82165 arabidopsis
267	6	3.4	71	2	Q8XGJ8	Q8XGJ8 salmonella	340	6	3.4	100	2	Q9LJV7	Q9LJV7 erwinia car
268	6	3.4	71	2	Q7COK5	Q7COK5 salmonella	341	6	3.4	100	2	Q6D9N2	Q6D9N2 thermoplaem
269	6	3.4	71	2	Q9UUI7	Q9UUI7 neisseria m	342	6	3.4	100	2	Q9H1P4	Q9H1P4 vesicular e
270	6	3.4	73	2	Q21096	Q21096 eurythemes	343	6	3.4	102	2	Q9H1P4	Q9H1P4 vesicular e
271	6	3.4	73	2	Q21096	Q7R95 plasmodium	344	6	3.4	102	2	Q88975	Q88975 vesicular e
272	6	3.4	74	2	Q7RGS5	Q8KY15 bacillus an	345	6	3.4	102	2	Q88976	Q88976 candida gla
273	6	3.4	74	2	Q8XKM1	Q9X6M1 klebsiella	346	6	3.4	103	2	Q6FLQ1	Q6FLQ1 trypanosoma
274	6	3.4	74	2	Q6E2J8	Q6E2J8 bacillus an	347	6	3.4	104	2	Q8WPP5	Q8WPP5 trypanosoma
275	6	3.4	75	2	Q72295	Q72295 caenorhabdi	348	6	3.4	104	2	Q8CAD9	Q8CAD9 arthrobacte
276	6	3.4	75	2	Q853Q4	Q853Q4 mycobacteri	349	6	3.4	104	2	Q8BD48	Q8BD48 synechococ
277	6	3.4	75	2	Q6LAL9	Q6LAL9 salmonella	350	6	3.4	106	2	Q8DH48	Q8DH48 shewanella
278	6	3.4	76	2	Q48209	Q48209 drosophila	351	6	3.4	107	2	Q8BNC2	Q8BNC2 mus musculu
279	6	3.4	76	2	Q48210	Q48210 drosophila	352	6	3.4	108	1	SY19_MOUSE	Q70460 mus musculu
280	6	3.4	76	2	Q48211	Q48211 drosophila	353	6	3.4	108	2	Q9UXJ3	Q9UXJ3 sulfolobus
281	6	3.4	76	2	Q48212	Q48212 drosophila	354	6	3.4	108	2	Q6RV30	Q6RV30 chironomus
282	6	3.4	76	2	Q48213	Q48213 drosophila	355	6	3.4	108	2	Q7RMT5	Q7RMT5 plasmodium
283	6	3.4	76	2	Q48214	Q48214 drosophila	356	6	3.4	108	2	Q7XP13	Q7XP13 oryza sativ
284	6	3.4	76	2	Q48215	Q48215 drosophila	357	6	3.4	108	2	Q8BNC2	Q8BNC2 mus musculu
285	6	3.4	76	2	Q48216	Q48216 drosophila	358	6	3.4	110	1	VLI_FPVLT	P6456 avian papill
286	6	3.4	76	2	Q48217	Q48217 drosophila	359	6	3.4	110	2	Q9H1B8	Q9H1B8 sulfolobus
287	6	3.4	76	2	Q48218	Q48218 drosophila	360	6	3.4	110	2	Q8H7A7	Q8H7A7 arabidopsis
288	6	3.4	76	2	Q48219	Q48219 drosophila	361	6	3.4	110	2	Q7NUP5	Q7NUP5 chromobacte
289	6	3.4	76	2	Q48220	Q48220 scaptomyza	362	6	3.4	110	2	Q6D2W2	Q6D2W2 erwinia car
290	6	3.4	76	2	Q48222	Q48222 drosophila	363	6	3.4	111	2	Q9VAR5	Q9VAR5 drosophila
291	6	3.4	76	2	Q48223	Q48223 drosophila	364	6	3.4	111	2	Q7NDB2	Q7NDB2 gloebacter
292	6	3.4	76	2	Q48224	Q48224 drosophila	365	6	3.4	112	2	Q9D634	Q9D634 m mus muscu
293	6	3.4	76	2	Q757G6	Q757G6 bacillus st	366	6	3.4	113	2	Q7Z6J7	Q7Z6J7 homo sapien
294	6	3.4	76	2	Q8GRL9	Q8GRL9 pseudomonas	367	6	3.4	114	2	Q9RK45	Q9RK45 streptomyce
295	6	3.4	76	2	P72914	P72914 synechocyst	368	6	3.4	114	2	Q8UD09	Q8UD09 agrobacteri
296	6	3.4	76	2	Q8UJ39	Q8UJ39 agrobacteri	369	6	3.4	115	2	Q9CQHO	Q9CQHO neurospora
297	6	3.4	76	2	Q9UTJ3	Q9UTJ3 neisseria m	370	6	3.4	115	2	Q6UY24	Q6UY24 homo sapien
298	6	3.4	77	2	Q6BGN6	Q6BGN6 debaryomyce	371	6	3.4	115	2	P95435	P95435 pseudomonas
299	6	3.4	77	2	Q7C9J9	Q7C9J9 rhizobium 1	372	6	3.4	115	2	Q7ZB07	Q7ZB07 desulfovibr
300	6	3.4	79	2	Q7C9J9	Q6uac6 anopheles g	373	6	3.4	115	2	Q8KX08	Q8KX08 proteus mlt
301	6	3.4	79	2	Q6UAT6	Q6uac6 bacterioph	374	6	3.4	116	2	Q73NB7	Q73NB7 tireponema d
302	6	3.4	79	2	Q9MB10	Q9mb10 bacterioph	375	6	3.4	116	2	Q73NB7	Q6d330 erwinia car
303	6	3.4	79	2	Q8A1S7	Q8a1s7 bacteroides	376	6	3.4	116	2	Q6D330	Q9YF43 aeropyrum p
304	6	3.4	80	1	YSPF_SHIFL	Q55298 shigella fl	377	6	3.4	117	2	Q9YF43	Q8Y08 aeropyrum p
305	6	3.4	81	2	Q24195	Q24195 oryza sativ	378	6	3.4	117	2	Q8YF08	Q8YF08 anabaena sp
306	6	3.4	82	2	Q7XAM4	Q7XAM4 brassica ra	379	6	3.4	117	2	Q6F6Y7	Q6F6Y7 acinetobact
307	6	3.4	82	2	Q83D70	Q83D70 coxiella bu	380	6	3.4	117	2	Q7U5E0	Q7U5E0 synechococ
308	6	3.4	82	2	Q711J8	Q711J8 lactobacilli	381	6	3.4	117	2	Q9KN10	Q9KN10 vibrio chol
309	6	3.4	84	1	PSAK_CYACA	Q19992 cyanidium c	382	6	3.4	118	2	Q9YR16	Q9YR16 aeropyrum p
310	6	3.4	84	1	Q8ZGN6	Q8ZGN6 yerstinia pe	383	6	3.4	119	2	Q84FRJ5	Q84FRJ5 uncultured
311	6	3.4	86	2	Q98A51	Q98A51 rhizobium 1	384	6	3.4	119	2	Q84FRJ5	Q84FRJ5 uncultured
312	6	3.4	88	2	Q42211	Q42211 arabidopsis	385	6	3.4	119	2	Q84FRJ7	Q84FRJ7 uncultured
313	6	3.4	88	2	Q30435	Q30435 enterococcu	386	6	3.4	119	2	Q84FRJ8	Q84FRJ8 uncultured
314	6	3.4	88	2	Q8NUY0	Q8NUY0 staphylococ	387	6	3.4	121	2	Q9OCZ4	Q9OCZ4 periplaneta
315	6	3.4	88	2	Q99RH6	Q99RH6 staphylococ	388	6	3.4	121	2	RL14_CHLMT	Q9QCZ4 chlamydia m
316	6	3.4	88	2	Q7A3P1	Q7A3P1 staphylococ	389	6	3.4	122	1	RL14_CHLMT	Q9QCZ4 chlamydia p
317	6	3.4	88	2	Q6G6L4	Q6G6L4 staphylococ	390	6	3.4	122	1	RL14_CHLMT	Q9QCZ4 chlamydia p
318	6	3.4	88	2	Q90YF5	Q90YF5 pleuronacte	391	6	3.4	122	1	Y202_MYCGB	Y202_MYCGB
319	6	3.4	89	1	GN1_XEMILA	P45656 xenopus lae	392	6	3.4	122	2	Q8L7Q8	Q8L7Q8 arabidopsis
320	6	3.4	89	2	Q8YCG5	Q8YCG5 bruceia me	393	6	3.4	122	2	Q73FQ3	Q73FQ3 wolbachia p
321	6	3.4	90	2	Q7YXO	Q7YXO mycobacteri	394	6	3.4	122	2	Q824P1	Q824P1 chlamydophi
322	6	3.4	90	2	Q7UMS2	Q7UMS2 rhodopirelli	395	6	3.4	122	2	Q6M553	Q6M553 parachlamyid
323	6	3.4	91	2	Q8LWAO	Q8LWAO ctus brucei	396	6	3.4	122	2	Q6M553	Q6M553 parachlamyid

397	6	3.4	123	2	Q7PN37	Q7PN37 anopheles g	470	6	3.4	138	2	Q8B186	Q8B186 san miguel
398	6	3.4	123	2	Q30533	Q30533 pseudomonas	471	6	3.4	139	2	Q6BT83	Q6BT83 debaryomyce
399	6	3.4	123	2	Q730V1	Q730V1 bacillus ce	472	6	3.4	139	2	Q6XH06	Q6XH06 drosophila
400	6	3.4	123	2	Q91329	Q91329 pseudomonas	473	6	3.4	139	2	Q9XK38	Q9XK38 drosophila
401	6	3.4	124	1	YBF3 YEAST	YBF3 baccharomyc	474	6	3.4	139	2	Q9XK53	Q9XK53 drosophila
402	6	3.4	124	2	Q7QVD9	Q7QVD9 giardia lam	475	6	3.4	139	2	Q9XN65	Q9XN65 drosophila
403	6	3.4	124	2	Q8B974	Q8B974 vesicular e	476	6	3.4	139	2	Q9XN66	Q9XN66 drosophila
404	6	3.4	125	2	Q97OK1	Q97OK1 sulfolobus	477	6	3.4	139	2	Q9XN67	Q9XN67 drosophila
405	6	3.4	125	2	Q9LH14	Q9LH14 arabidopsis	478	6	3.4	139	2	Q9XN68	Q9XN68 drosophila
406	6	3.4	125	2	Q66GZ4	Q66GZ4 xenopus lae	479	6	3.4	139	2	Q9XN69	Q9XN69 drosophila
407	6	3.4	126	2	Q9G919	Q9G919 rana chensui	480	6	3.4	139	2	Q9XN70	Q9XN70 drosophila
408	6	3.4	126	2	Q8CT85	Q8CT85 staphylococ	481	6	3.4	139	2	Q9XN71	Q9XN71 drosophila
409	6	3.4	126	2	Q9PDL3	Q9PDL3 xyella fas	482	6	3.4	139	2	Q9XN85	Q9XN85 drosophila
410	6	3.4	127	2	Q9ZU00	Q9ZU00 arabidopsis	483	6	3.4	139	2	Q9XN86	Q9XN86 drosophila
411	6	3.4	127	2	Q64VZ6	Q64VZ6 bacteroides	484	6	3.4	139	2	Q9XN87	Q9XN87 drosophila
412	6	3.4	127	2	Q8UT13	Q8UT13 agrobacteri	485	6	3.4	139	2	Q9XN88	Q9XN88 drosophila
413	6	3.4	127	2	Q97JK9	Q97JK9 clostridium	486	6	3.4	139	2	Q33304	Q33304 mycobacteri
414	6	3.4	127	2	Q7A1C1	Q7A1C1 staphylococ	487	6	3.4	139	2	Q735J7	Q735J7 bacillus ce
415	6	3.4	127	2	Q7A2T4	Q7A2T4 staphylococ	488	6	3.4	139	2	Q8B185	Q8B185 san miguel
416	6	3.4	127	2	Q7A612	Q7A612 staphylococ	489	6	3.4	140	2	Q65NM6	Q65NM6 bacillus 11
417	6	3.4	127	2	Q8B8U6	Q8B8U6 lactobacill	490	6	3.4	141	1	YCB6_PSEDE	YCB6_PSEDE
418	6	3.4	127	2	Q9ZNG7	Q9ZNG7 staphylococ	491	6	3.4	141	2	Q9YE51	Q9YE51 aeropyrum p
419	6	3.4	127	2	Q6GAX3	Q6GAX3 staphylococ	492	6	3.4	141	2	Q9HXQ3	Q9HXQ3 pseudomonas
420	6	3.4	127	2	Q6G1D5	Q6G1D5 staphylococ	493	6	3.4	141	2	Q9ZFM9	Q9ZFM9 fusobacteri
421	6	3.4	128	2	Q8TM72	Q8TM72 methanosarc	494	6	3.4	142	1	HBA_CARAU	HBA_CARAU
422	6	3.4	128	2	Q6WFF6	Q6WFF6 human immun	495	6	3.4	143	2	Q9ZMU9	Q9ZMU9 helicobacte
423	6	3.4	129	2	Q7YU27	Q7YU27 trypanosoma	496	6	3.4	143	2	Q8TH84	Q8TH84 ctenopharym
424	6	3.4	129	2	P95131	P95131 mycobacteri	497	6	3.4	143	2	Q8TH90	Q8TH90 carassius a
425	6	3.4	129	2	Q7RX15	Q7RX15 mycobacteri	498	6	3.4	144	1	CND8_HUMAN	CND8_HUMAN
426	6	3.4	131	2	Q7RZ15	Q7RZ15 neurospora	499	6	3.4	144	2	Q6KD68	Q6KD68 escherichia
427	6	3.4	131	2	Q75J22	Q75J22 dictyosteli	500	6	3.4	144	2	Q7VJR6	Q7VJR6 helicobacte
428	6	3.4	131	2	Q6VAG5	Q6VAG5 bacteroides	501	6	3.4	144	2	Q8E514	Q8E514 streptococc
429	6	3.4	131	2	Q6MLX3	Q6MLX3 bdellovibri	502	6	3.4	144	2	Q8EKK4	Q8EKK4 oceanobacil
430	6	3.4	133	2	Q9YDU6	Q9YDU6 aeropyrum p	503	6	3.4	144	2	Q9ANE2	Q9ANE2 bradyrhizob
431	6	3.4	135	2	Q6FUG3	Q6FUG3 homo saplen	504	6	3.4	144	2	Q9UAST	Q9UAST agrobacteri
432	6	3.4	135	2	Q7RUV7	Q7RUV7 prochloroco	505	6	3.4	145	2	Q8FV83	Q8FV83 bruceella su
433	6	3.4	137	2	Q8BMR4	Q8BMR4 corynebacte	506	6	3.4	145	2	Q8BUL5	Q8BUL5 xanthomonas
434	6	3.4	137	2	Q8BUT5	Q8BUT5 bradyrhizob	507	6	3.4	145	2	Q6D2C8	Q6D2C8 erwina car
435	6	3.4	138	2	Q8SAR0	Q8SAR0 drosophila	508	6	3.4	145	2	Q8BY58	Q8BY58 mus musculu
436	6	3.4	138	2	Q8SAR1	Q8SAR1 drosophila	509	6	3.4	146	2	Q8J1X8	Q8J1X8 coccidioido
437	6	3.4	138	2	Q8ST71	Q8ST71 drosophila	510	6	3.4	146	2	Q7X650	Q7X650 oryza sativ
438	6	3.4	138	2	Q8ST72	Q8ST72 drosophila	511	6	3.4	146	2	Q9M719	Q9M719 arabidopsis
439	6	3.4	138	2	Q8ST73	Q8ST73 drosophila	512	6	3.4	146	2	Q8P866	Q8P866 xanthomonas
440	6	3.4	138	2	Q8ST74	Q8ST74 drosophila	513	6	3.4	146	2	Q8PUL5	Q8PUL5 xanthomonas
441	6	3.4	138	2	Q8ST75	Q8ST75 drosophila	514	6	3.4	147	1	HPK_PORCI	HPK_PORCI
442	6	3.4	138	2	Q8ST77	Q8ST77 drosophila	515	6	3.4	148	2	Q6GWT5	Q6GWT5 homo saplen
443	6	3.4	138	2	Q8ST78	Q8ST78 drosophila	516	6	3.4	148	2	Q9VBG7	Q9VBG7 drosophila
444	6	3.4	138	2	Q8ST79	Q8ST79 drosophila	517	6	3.4	148	2	Q6YRL5	Q6YRL5 oryza sativ
445	6	3.4	138	2	Q8ST80	Q8ST80 drosophila	518	6	3.4	148	2	Q8J1L9	Q8J1L9 streptomyce
446	6	3.4	138	2	Q8ST81	Q8ST81 drosophila	519	6	3.4	149	2	Q09784	Q09784 san miguel
447	6	3.4	138	2	Q8ST82	Q8ST82 drosophila	520	6	3.4	149	2	Q09787	Q09787 san miguel
448	6	3.4	138	2	Q8ST83	Q8ST83 drosophila	521	6	3.4	149	2	Q8UZU1	Q8UZU1 bovine cali
449	6	3.4	138	2	Q8ST84	Q8ST84 drosophila	522	6	3.4	150	2	Q8PFL1	Q8PFL1 xanthomonas
450	6	3.4	138	2	Q8ST86	Q8ST86 drosophila	523	6	3.4	150	2	Q09736	Q09736 cetacean ca
451	6	3.4	138	2	Q8ST87	Q8ST87 drosophila	524	6	3.4	150	2	Q09775	Q09775 primate cal
452	6	3.4	138	2	Q8ST88	Q8ST88 drosophila	525	6	3.4	150	2	Q09776	Q09776 repelle cal
453	6	3.4	138	2	Q8ST89	Q8ST89 drosophila	526	6	3.4	150	2	Q09785	Q09785 san miguel
454	6	3.4	138	2	Q8ST91	Q8ST91 drosophila	527	6	3.4	150	2	Q09786	Q09786 san miguel
455	6	3.4	138	2	Q8ST92	Q8ST92 hirtodrosop	528	6	3.4	151	2	Q9VBF0	Q9VBF0 drosophila
456	6	3.4	138	2	Q8ST93	Q8ST93 drosophila	529	6	3.4	151	2	Q9C760	Q9C760 arabidopsis
457	6	3.4	138	2	Q8ST96	Q8ST96 drosophila	530	6	3.4	151	2	Q9EF07	Q9EF07 arabidopsis
458	6	3.4	138	2	Q8ST98	Q8ST98 drosophila	531	6	3.4	152	2	Q7PJ06	Q7PJ06 anopheles g
459	6	3.4	138	2	Q9TAV8	Q9TAV8 drosophila	532	6	3.4	152	2	Q84JN5	Q84JN5 oryza sativ
460	6	3.4	138	2	Q9TAV9	Q9TAV9 drosophila	533	6	3.4	152	2	Q61BB7	Q61BB7 oligotropha
461	6	3.4	138	2	Q9TAW0	Q9TAW0 drosophila	534	6	3.4	152	2	Q8WH39	Q8WH39 agrobacteri
462	6	3.4	138	2	Q9TAW1	Q9TAW1 drosophila	535	6	3.4	153	1	RISC_ARCFU	RISC_ARCFU
463	6	3.4	138	2	Q9TAW2	Q9TAW2 drosophila	536	6	3.4	153	2	Q647X1	Q647X1 uncultured
464	6	3.4	138	2	Q9XJY8	Q9XJY8 drosophila	537	6	3.4	153	2	Q61LV3	Q61LV3 drosophila
465	6	3.4	138	2	Q9XK12	Q9XK12 drosophila	538	6	3.4	153	2	Q8P3Z0	Q8P3Z0 xanthomonas
466	6	3.4	138	2	Q9XN53	Q9XN53 drosophila	539	6	3.4	153	2	Q9AA58	Q9AA58 caulobacter
467	6	3.4	138	2	Q9XN54	Q9XN54 drosophila	540	6	3.4	153	2	Q90068	Q90068 feline immu
468	6	3.4	138	2	Q9XN55	Q9XN55 drosophila	541	6	3.4	154	2	Q9HL56	Q9HL56 thermoplasma
469	6	3.4	138	2	Q8BJJ3	Q8BJJ3 shewanella	542	6	3.4	154	2	Q8YHN9	Q8YHN9 bruceella me

543	6	3.4	154	2	06G0D3	08G0d3 bruceella su	616	6	3.4	170	2	07MC16	07mc16 vibrio vuln
544	6	3.4	154	2	06C238	06c238 erwinia car	617	6	3.4	170	2	08D5K2	08d5k2 vibrio vuln
545	6	3.4	155	2	08XM89	08xm89 clostridium	618	6	3.4	171	1	1126_HUMAN	09npb9 homo sapien
546	6	3.4	155	2	06UG70	06ug70 sulfolobus	619	6	3.4	172	1	0824V3	0824v3 chlamydomo
547	6	3.4	156	2	08SCM0	08scm0 pseudomonas	620	6	3.4	172	2	091749	091749 pseudomonas
548	6	3.4	156	2	09S6G3	09s6g3 streptococc	621	6	3.4	173	1	BURS_DROME	09y4d3 drosophila
549	6	3.4	156	2	09S6G4	09s6g4 streptococc	622	6	3.4	173	1	CD3D_MOUSE	P04235 mus musculu
550	6	3.4	157	1	09DHW7	09dhw7 yaba-like d	623	6	3.4	173	1	YK01_YEAST	P36067 saccharomyc
551	6	3.4	157	1	LSPA_HELPY	P25178 helicobacte	624	6	3.4	173	1	07RNT2	07rnt2 plasmidum
552	6	3.4	157	2	06L3W7	06l3w7 solanum dem	625	6	3.4	173	2	06T7L1	06t7l1 oryza sativ
553	6	3.4	157	2	09S006	09s006 helicobacte	626	6	3.4	173	2	06Q0V6	06q0v6 uncultured
554	6	3.4	157	2	082106	082106 streptomyce	627	6	3.4	173	2	07WX23	07wx23 alcaligenes
555	6	3.4	157	2	08A305	08a305 bacterioides	628	6	3.4	173	2	08RBF3	08rbf3 thermocaneer
556	6	3.4	157	2	010694	010694 avian papil	629	6	3.4	173	2	083E94	083e94 coxiella bu
557	6	3.4	158	1	RK12_ORYSA	022386 oryza sativ	630	6	3.4	173	2	06S398	06s398 mus musculu
558	6	3.4	158	2	09XSA0	09xsa0 ovine aries	631	6	3.4	173	2	06S398	06s398 bovine call
559	6	3.4	158	2	09SCS5	09scs5 arabidopsis	632	6	3.4	173	2	087003	087003 skunk calic
560	6	3.4	158	2	09EMB3	09emb3 streptomyce	633	6	3.4	173	2	087005	087005 skunk calic
561	6	3.4	158	2	08NXC0	08nxc0 staphylococ	634	6	3.4	173	2	087007	087007 skunk calic
562	6	3.4	158	2	06N7D7	06n7d7 rhodospseudo	635	6	3.4	173	2	087018	087018 skunk calic
563	6	3.4	159	1	VT3A_CAPVI	P48276 cyanophora	636	6	3.4	173	2	088174	088174 san miguel
564	6	3.4	159	1	YC36_CVAPA	P48276 cyanophora	637	6	3.4	173	2	088176	088176 san miguel
565	6	3.4	159	2	06SE59	06se59 verticillium	638	6	3.4	173	2	088183	088183 san miguel
566	6	3.4	159	2	06ESF0	06esf0 verticillium	639	6	3.4	173	2	088965	088965 vesicular e
567	6	3.4	159	2	08YVL5	08yvl5 anabaena sp	640	6	3.4	173	2	088973	088973 homo sapien
568	6	3.4	159	2	08YVL5	08yvl5 anabaena sp	641	6	3.4	174	2	08WX55	08wx55 homo sapien
569	6	3.4	159	2	08YVL5	08yvl5 anabaena sp	642	6	3.4	174	2	092VR1	092vr1 rhizobium m
570	6	3.4	160	2	0910J8	0910j8 lumpy skin	643	6	3.4	174	2	092VR1	092vr1 rhizobium m
571	6	3.4	160	2	08U2B6	08u2b6 pyrococcus	644	6	3.4	175	2	06ZS55	06z555 homo sapien
572	6	3.4	160	2	0610T4	0610t4 picornavirus	645	6	3.4	175	2	08E1F2	08e1f2 streptococc
573	6	3.4	160	2	07RP05	07rp05 plasmodium	646	6	3.4	175	2	08B6X0	08b6x0 streptococc
574	6	3.4	160	2	08PNC3	08pnc3 xanthomonas	647	6	3.4	176	2	070M7	070m7 crassostrea
575	6	3.4	160	2	08YCY2	08ycy2 bruceella me	648	6	3.4	176	2	071DQ8	071dq8 lobochlamys
576	6	3.4	161	1	08YCY2	08ycy2 bruceella me	649	6	3.4	176	2	072S24	072s24 tetraodon n
577	6	3.4	161	1	TATE_SPRCO	09h157 thermoplasma	650	6	3.4	177	1	IL19_HUMAN	09und0 homo sapien
578	6	3.4	161	2	09HL57	09hl57 thermoplasma	651	6	3.4	177	1	06FA57	06fa57 pluteella xy
579	6	3.4	161	2	09HL57	09hl57 thermoplasma	652	6	3.4	177	1	COX2_RICPR	09zdm3 rickettsia
580	6	3.4	161	2	09HL57	09hl57 thermoplasma	653	6	3.4	178	2	032584	032584 escherichia
581	6	3.4	162	1	PHAI_PREDI	088439 streptococ	654	6	3.4	178	2	08FR96	08fr96 coynebacte
582	6	3.4	162	1	PHAI_PREDI	P07122 streptococ	655	6	3.4	178	2	09KPB5	09kpb5 vibrio chol
583	6	3.4	162	1	PHAI_PREDI	P14876 streptococ	656	6	3.4	180	2	08PVJ2	08pvj2 methanosarc
584	6	3.4	163	1	LSPA_HELPY	09zmx3 helicobacte	657	6	3.4	180	2	06UB88	06ub88 staphylococ
585	6	3.4	163	2	06ZRX9	06zrx9 homo sapien	658	6	3.4	180	2	07CS40	07cs40 agrobacteri
586	6	3.4	163	2	07PRJ0	07prj0 anopheles g	659	6	3.4	180	2	08XRY8	08xry8 ralteonria s
587	6	3.4	163	2	08H3A5	08h3a5 schistosoma	660	6	3.4	180	2	08CKX9	08ckx9 oceanobacil
588	6	3.4	163	2	07TTN0	07ttn0 haemophilus	661	6	3.4	181	2	077311	077311 cyprinus ca
589	6	3.4	163	2	09CQ09	09cq09 m mus muscu	662	6	3.4	181	2	09X826	09x826 streptomyce
590	6	3.4	163	2	09CQ09	09cq09 m mus muscu	663	6	3.4	181	2	09X826	09x826 streptomyce
591	6	3.4	164	2	08S988	08s988 sphingomonas	664	6	3.4	181	2	088187	088187 san miguel
592	6	3.4	164	2	07BKRO	07bkro synecocyst	665	6	3.4	182	2	07Q098	07q098 giardia lam
593	6	3.4	164	2	09KJH5	09kh5 synecocyst	666	6	3.4	182	2	0902G7	0902g7 caenorhabdi
594	6	3.4	165	2	06STB6	06stb6 cereal yell	667	6	3.4	182	2	08XHG7	08xhg7 clostridium
595	6	3.4	165	2	07NMB7	07nmb7 gloebacter	668	6	3.4	183	2	08U878	08u878 agrobacteri
596	6	3.4	166	2	08Y9D0	08y9d0 listeria mo	669	6	3.4	183	2	045250	045250 caenorhabdi
597	6	3.4	166	2	092B50	092b50 listeria in	670	6	3.4	183	2	08W760	08w760 bacterioph
598	6	3.4	166	2	0722U8	0722u8 listeria mo	671	6	3.4	183	2	08W760	08w760 bacterioph
599	6	3.4	166	2	07V6R8	07v6r8 prochloroco	672	6	3.4	183	2	0921D2	0921d2 chlamydomo
600	6	3.4	167	1	CD3D_SHEEP	081438 ovine aries	673	6	3.4	183	2	0822U3	0822u3 homo sapien
601	6	3.4	167	1	08LDI5	08ldi5 arabidopsis	674	6	3.4	184	1	TR17_HUMAN	06pe46 homo sapien
602	6	3.4	167	2	09SACS	09sacs arabidopsis	675	6	3.4	184	1	06PE46	06pe46 homo sapien
603	6	3.4	167	2	07W063	07w063 bordetella	676	6	3.4	184	2	06NEZ6	06nez6 rhodospendo
604	6	3.4	167	2	07W3S8	07w3s8 bordetella	677	6	3.4	184	2	07UXK6	07uxk6 rhodopirell
605	6	3.4	167	2	07WFS6	07wfs6 bordetella	678	6	3.4	184	2	08ENH8	08enh8 oceanobacil
606	6	3.4	168	2	08SNF7	08snf7 xiphophorus	679	6	3.4	184	2	08ENH8	08enh8 oceanobacil
607	6	3.4	168	2	08SNF3	08snf3 xiphophorus	680	6	3.4	185	1	AP10_HUMAN	09um13 mus musculu
608	6	3.4	168	2	08SNF4	08snf4 xiphophorus	681	6	3.4	185	1	AP10_HUMAN	09um13 mus musculu
609	6	3.4	168	2	08SNF5	08snf5 xiphophorus	682	6	3.4	185	1	09VAF7	09vaf7 haemophilus
610	6	3.4	168	2	08SNF6	08snf6 xiphophorus	683	6	3.4	185	2	09ZWF4	09zwf4 oryza sativ
611	6	3.4	168	2	08SNF6	08snf6 xiphophorus	684	6	3.4	185	2	09ZWF4	09zwf4 oryza sativ
612	6	3.4	169	1	YCE0342	090342 cercoptichec	685	6	3.4	185	2	072T61	072t61 leptospira
613	6	3.4	169	1	YCE0342	090342 cercoptichec	686	6	3.4	185	2	074IK7	074ik7 leptospira
614	6	3.4	169	1	08SNF7	08snf7 xiphophorus	687	6	3.4	185	2	08P292	08p292 leptospira
615	6	3.4	169	2	068613	068613 synecococc	688	6	3.4	186	2	08NPE4	08np44 coynebacte

689	3.4	186	2	Q7ND30	Q7nd30 gloeobacter	762	6	3.4	200	2	Q66CW4	Q66cw4 yersinia ps
690	3.4	186	2	Q6BJ57	Q6bj57 gopherus po	763	6	3.4	200	2	Q90YF1	Q90yf1 pleuronecte
691	3.4	187	2	Q6XJ2P4	Q6xj2f4 verticordia	764	6	3.4	202	1	RB13_MOUSE	Q94d03 mus musculu
692	3.4	187	2	Q6X2F8	Q6x2f8 chameleau	765	6	3.4	202	1	V357_CAMB	Q991e4 campylobact
693	3.4	187	2	Q6X2F8	Q6x2f8 chameleau	766	6	3.4	202	2	Q61700	Q61700 pyrobaculum
694	3.4	187	2	Q9HVS2	Q9hvs2 pseudomonas	767	6	3.4	202	2	Q703Z8	Q703z8 thermoprote
695	3.4	188	1	COX2_RICCN	Q92112 rickettsia	768	6	3.4	202	2	Q970X9	Q970x9 sulfolobus
696	3.4	188	2	O27534	O27534 methanobact	769	6	3.4	202	2	Q6EQ71	Q6eq71 oryza sativ
697	3.4	188	2	Q6CGN2	Q6cgn2 yarrowia li	770	6	3.4	202	2	Q9RG18	Q9rg18 bacteroides
698	3.4	188	2	Q7YX04	Q7yx04 caenorhabdi	771	6	3.4	202	2	Q9RPA8	Q9rpa8 streptomyc
699	3.4	188	2	Q6AVC7	Q6avc7 oryza sativ	772	6	3.4	202	2	Q64VS8	Q64vs8 bacteroides
700	3.4	188	2	Q7PBB0	Q7pbb0 rickettsia	773	6	3.4	203	1	GTSL_BLAG	O15598 blactella g
701	3.4	188	2	Q72Y14	Q72y14 bacillus ce	774	6	3.4	203	1	HIS5_THETN	O18583 thermomater
702	3.4	188	2	O816S6	O816s6 bacillus ce	775	6	3.4	203	2	Q681Z2	Q681z2 arabidopsis
703	3.4	188	2	O81KX2	O81kx2 bacillus an	776	6	3.4	203	2	Q7AB11	Q7ab11 escherichia
704	3.4	188	2	Q6HBO2	Q6hbq2 bacillus th	777	6	3.4	203	2	Q7VP8	Q7vp8 bordetella
705	3.4	188	2	Q6HCD8	Q6hcd8 bacillus th	778	6	3.4	203	2	Q7WAS5	Q7was5 bordetella
706	3.4	188	2	O8R334	O8r334 mus musculu	779	6	3.4	203	2	Q7WY14	Q7wy14 bordetella
707	3.4	189	2	O8KD20	O8kd20 chlorobium	780	6	3.4	204	1	COAT_BYDVN	P27578 barley yell
708	3.4	189	2	O8PF77	O8pf77 xanthomonas	781	6	3.4	204	1	GBIR_HUMN	P52565 homo sapien
709	3.4	189	2	O8USG7	O8usg7 agrobacteri	782	6	3.4	204	2	Q8TQ03	Q8tcq3 mechanosarc
710	3.4	190	2	Q6DHH7	Q6dhh7 brachydanti	783	6	3.4	204	2	O8VZ03	O8vzq3 arabidopsis
711	3.4	191	2	Q9LH47	Q9lh47 arabidopsis	784	6	3.4	204	2	Q9SHH9	Q9shh9 arabidopsis
712	3.4	191	2	Q7NM10	Q7nm10 chymobacte	785	6	3.4	204	2	O8X819	O8x819 escherichia
713	3.4	192	1	G1DB_MYCGE	P47620 mycoplasma	786	6	3.4	204	2	Q91ZF3	Q91zf3 cereal yell
714	3.4	192	2	O6L012	O6l012 picophilus	787	6	3.4	206	1	NO21_SOYBN	P16313 glycine max
715	3.4	192	2	P95975	P95975 sulfolobus	788	6	3.4	207	1	PR1_HYPMO	P33595 hypophthalm
716	3.4	192	2	O6C9M1	O6c9m1 yarrowia li	789	6	3.4	207	2	Q7PL02	Q7pl02 anophelies g
717	3.4	192	2	Q7KXW7	Q7kxw7 oryza sativ	790	6	3.4	207	2	Q9ABCI	Q9abp1 desulfitoba
718	3.4	192	2	O52373	O52373 pseudomonas	791	6	3.4	207	2	O8KRC0	O8krc0 chlorobium
719	3.4	192	2	Q7V0V4	Q7vov4 prochloroco	792	6	3.4	207	2	Q7MSQ4	Q7mq4 wolfinella s
720	3.4	193	2	O8WYU3	O8wyu3 homo sapien	793	6	3.4	208	2	O61GL9	O61gl9 drosophila
721	3.4	193	2	O9RX05	O9rx05 deinococcus	794	6	3.4	208	2	O666F9	O666f9 vibrio chol
722	3.4	194	1	PTH_PASMU	P57820 pasteurella	795	6	3.4	208	2	O8X0S0	O8x0s0 raietonia s
723	3.4	194	2	O8IQ56	O8iq56 drosophila	796	6	3.4	210	2	O95XL4	O95xl4 caenorhabdi
724	3.4	194	2	O634A5	O634a5 gliosina mo	797	6	3.4	210	2	O245E7	O245e7 zea mays (m
725	3.4	194	2	O8LBB9	O8lbb9 arabidopsis	798	6	3.4	210	2	O89Z42	O89z42 bacteroides
726	3.4	194	2	O6Z366	O6z366 oryza sativ	799	6	3.4	211	2	O8IMY2	O8imy2 drosophila
727	3.4	194	2	O9SD84	O9s84 arabidopsis	800	6	3.4	211	2	Q7PGA2	Q7pga2 anophelies g
728	3.4	194	2	O82B21	O82b21 streptomyc	801	6	3.4	212	2	O67MM8	O67mm8 oryza sativ
729	3.4	195	2	O97416	O97416 sulfolobus	802	6	3.4	212	2	O9PK98	O9pk98 arabidopsis
730	3.4	195	2	O9NT21	O9nt21 homo sapien	803	6	3.4	212	2	O6G591	O6g591 bartonella
731	3.4	195	2	O8MUR9	O8mur9 anophelies g	804	6	3.4	213	1	YMO6_YEAST	O04477 saccharomyc
732	3.4	195	2	Q7YT05	Q7yq5 caenorhabdi	805	6	3.4	213	2	O8YNH8	O8ynh8 anabaena sp
733	3.4	195	2	Q7F2F2	Q7f2f2 oryza sativ	806	6	3.4	214	2	O8PUU0	O8puu0 mechanosarc
734	3.4	196	2	O9VUM4	O9vum4 drosophila	807	6	3.4	214	2	O05387	O05387 saccharomyc
735	3.4	196	2	O44751	O44751 borrelia bu	808	6	3.4	214	2	O6ST01	O6std1 manheimia
736	3.4	196	2	O6LKW7	O6lkw7 photodacter	809	6	3.4	214	2	Q72B98	Q72b98 desulfotibr
737	3.4	196	2	O8DCM4	O8dcm4 vibrio vuln	810	6	3.4	214	2	Q7WAD1	Q7wad1 bordetella
738	3.4	196	2	O9HZR6	O9hzr6 pseudomonas	811	6	3.4	214	2	Q7WJH3	Q7wjh3 bordetella
739	3.4	197	1	VHR2_CAPVK	P19747 capripoxvir	812	6	3.4	216	2	O6PNG9	O6png9 uncultured
740	3.4	197	2	O6CB54	O6cb54 yarrowia li	813	6	3.4	217	2	O8CRC4	O8crc4 homo sapien
741	3.4	197	2	O9VZP1	O9vzp1 drosophila	814	6	3.4	217	2	O82GR6	O82gr6 streptomyc
742	3.4	197	2	O8Y7N2	O8y7n2 listeria mo	815	6	3.4	217	2	O89BP9	O89bp9 bradyrhizob
743	3.4	197	2	O92CG6	O92cg6 listeria in	816	6	3.4	217	2	O9X5C4	O9x5c4 streptococc
744	3.4	197	2	O92T19	O92t19 rhizobium m	817	6	3.4	218	1	GTS_ANOGA	P46428 anophelies g
745	3.4	197	2	Q720I3	Q720i3 listeria mo	818	6	3.4	218	2	O6PEG3	O6peg3 homo sapien
746	3.4	197	2	O8BRM1	O8brm1 mycoplasma	819	6	3.4	218	2	O8LEB1	O8leb1 arabidopsis
747	3.4	197	2	O8KOK8	O8kok8 mus musculu	820	6	3.4	218	2	Q93XZ7	Q93xz7 arabidopsis
748	3.4	197	2	O8JUT1	O8jut1 lumpy skin	821	6	3.4	218	2	O8ID53	O8id53 bacillus ce
749	3.4	197	2	O8JUT6	O8jut6 lumpy skin	822	6	3.4	218	2	O6HGF1	O6hgf1 bacillus th
750	3.4	197	2	Q7THD0	Q7thd0 capripoxvir	823	6	3.4	219	2	O635P2	O635p2 bacillus ce
751	3.4	198	1	P8T2_YEAST	O12335 saccharomyc	824	6	3.4	219	2	Q731R1	Q731r1 bacillus ce
752	3.4	198	1	VHR2_LSDV	O91mu3 lumpy skin	825	6	3.4	219	2	O81MU1	O81mj1 bacillus an
753	3.4	198	2	O6FM13	O6fm13 candida gla	826	6	3.4	219	2	O89Z24	O89z24 bacteroides
754	3.4	198	2	O857J9	O857j9 mycobacteri	827	6	3.4	219	2	O6HEC8	O6hec8 bacillus th
755	3.4	198	2	O7PS93	O7ps93 sorghum bic	828	6	3.4	220	1	YF09_HELPJ	O94jbl helicobacte
756	3.4	198	2	O8YNH6	O8ynh6 anabaena sp	829	6	3.4	220	1	YF09_HELPJ	O26039 helicobacte
757	3.4	198	2	O89B11	O89b11 bradyrhizob	830	6	3.4	220	2	O7QDT1	O7qdt1 anophelies g
758	3.4	199	2	O6M0F6	O6mf6 mechanococc	831	6	3.4	220	2	O7XJ12	O7xj12 oryza sativ
759	3.4	199	2	O9M8S1	O9ms1 arabidopsis	832	6	3.4	220	2	Q7X1N0	Q7x1n0 leptocptiri
760	3.4	199	2	O8XHN9	O8xhn9 clostridium	833	6	3.4	220	2	O9F5G6	O9f5g6 agrobacteri
761	3.4	199	2	O6N4G9	O6n4g9 rhodopseudo	834	6	3.4	220	2	Q92QW3	Q92qw3 rhizobium m



835	6	3.4	220	2	Q72H14	Q72h14 thermus the	908	6	3.4	237	2	Q651C1	Q651c1 oryza sativ
836	6	3.4	220	2	Q73MF5	Q73mf5 treponema d	909	6	3.4	237	2	Q7P6D4	Q7P6d4 fusobacteri
837	6	3.4	221	2	Q8E7J3	Q8E7j3 streptococc	910	6	3.4	237	2	Q9F0X5	Q9F0x5 pseudomonas
838	6	3.4	222	2	Q8IX38	Q8IX38 homo sapien	911	6	3.4	237	2	Q8KH02	Q8KH02 mus musculu
839	6	3.4	222	2	Q9G9D8	Q9G9d8 ascaphus tr	912	6	3.4	238	2	Q6CV44	Q6CV44 kluyveromyc
840	6	3.4	223	2	Q7NSH4	Q7NSH4 streptomyce	913	6	3.4	238	2	Q7Z5X6	Q7Z5x6 homo sapien
841	6	3.4	223	2	Q9L2I8	Q9L2I8 streptomyce	914	6	3.4	238	2	Q9Z5W3	Q9Z5w3 pseudomonas
842	6	3.4	224	2	Q7OD44	Q7OD44 saccharomyc	915	6	3.4	238	2	Q67863	Q67863 aquifex aeo
843	6	3.4	224	2	Q7OD47	Q7OD47 saccharomyc	916	6	3.4	238	2	Q61NV3	Q61nv3 xenopus lae
844	6	3.4	224	2	Q7ODB2	Q7ODb2 saccharomyc	917	6	3.4	239	2	Q8MU22	Q8MU22 homo sapien
845	6	3.4	224	2	Q8YA47	Q8YA47 listeria mo	918	6	3.4	239	2	Q9X5C5	Q9X5c5 streptococc
846	6	3.4	224	2	Q9ZEW8	Q9ZEW8 listeria in	919	6	3.4	239	2	Q92ZJ4	Q92Zj4 rhizobium m
847	6	3.4	224	2	Q97FM6	Q97fm6 clostridium	920	6	3.4	239	2	Q6ST87	Q6ST87 cereal yell
848	6	3.4	224	2	Q7J3Z2	Q7J3z2 listeria mo	921	6	3.4	240	2	Q96DY3	Q96dy3 homo sapien
849	6	3.4	225	2	Q96KH5	Q96kh5 homo sapien	922	6	3.4	240	2	Q6S2C9	Q6S2c9 homo sapien
850	6	3.4	226	1	YCKA_BACSU	P42399 bacillus su	923	6	3.4	240	2	Q9V402	Q9V402 drosophila
851	6	3.4	227	1	COX2_HALGR	P38596 halichoerus	924	6	3.4	240	2	Q8VTU0	Q8VTU0 listeria mo
852	6	3.4	227	1	COX2_PROVI	000528 phoca vitul	925	6	3.4	240	2	Q6M1L1	Q6M1l1 bdellovibri
853	6	3.4	227	2	Q679G9	Q679g9 muscela vis	926	6	3.4	240	2	Q6NDW9	Q6ndw9 rhodospseud
854	6	3.4	227	2	Q679H0	Q679h0 guilo guilo	927	6	3.4	240	2	Q71MS7	Q71ms7 listeria mo
855	6	3.4	227	2	Q679H4	Q679h4 phoca largh	928	6	3.4	240	2	Q90WT2	Q90wt2 brachydanio
856	6	3.4	227	2	Q679H5	Q679h5 phoca hisp	929	6	3.4	240	2	Q61QV5	Q61qv5 brachydanio
857	6	3.4	227	2	Q679H6	Q679h6 phoca groen	930	6	3.4	241	2	Q6LKY0	Q6LKY0 photobacter
858	6	3.4	227	2	Q679H7	Q679h7 cytophoxa	931	6	3.4	241	2	Q7V7E3	Q7V7e3 prochloroco
859	6	3.4	227	2	Q679H8	Q679h8 erignathus	932	6	3.4	241	2	Q8Z6R4	Q8Z6r4 streptomyce
860	6	3.4	227	2	Q679H9	Q679h9 monachus sc	933	6	3.4	241	2	Q89C05	Q89c05 bradyrhizob
861	6	3.4	227	2	Q679I0	Q679i0 monachus sc	934	6	3.4	242	1	FLIG_SHIBO	FLIG_SHIBO
862	6	3.4	227	2	Q679I1	Q679i1 mirounga le	935	6	3.4	242	2	Q9G9D7	Q9G9d7 ascaphus tr
863	6	3.4	227	2	Q679I5	Q679i5 leprocyhot	936	6	3.4	242	2	Q40670	Q40670 oryza sativ
864	6	3.4	227	2	Q679I6	Q679i6 hydrurga le	937	6	3.4	242	2	Q8C6S8	Q8C6s8 mus musculu
865	6	3.4	227	2	Q679I8	Q679i8 ommatophoca	938	6	3.4	243	1	GCTR_HUMAN	GCTR_HUMAN
866	6	3.4	227	2	Q679J0	Q679j0 lobodon car	939	6	3.4	244	2	Q61B75	Q61b75 homo sapien
867	6	3.4	227	2	Q9LHX1	Q9Lhx1 oryza sativ	940	6	3.4	244	2	Q65ZC8	Q65zc8 homo sapien
868	6	3.4	227	2	Q8RPE9	Q8rpe9 legionella	941	6	3.4	245	1	T2M4_METJA	T2M4_METJA
869	6	3.4	227	2	Q65NM3	Q65nm3 bacillus li	942	6	3.4	245	2	Q8ZMB3	Q8Zmb3 pyrobaculum
870	6	3.4	227	2	Q9PMW3	Q9pmw3 campylobact	943	6	3.4	245	2	Q6CAL5	Q6cal5 giardia lam
871	6	3.4	227	2	Q9YGT6	Q9ygt6 brachydantio	944	6	3.4	245	2	Q7QZ93	Q7Qz93 macaca faec
872	6	3.4	228	1	PCAI_ACTIAD	Q43973 acinetobact	945	6	3.4	245	2	Q95LW2	Q95lw2 alcaligenes
873	6	3.4	228	2	Q52047	Q52047 plasmid phv	946	6	3.4	245	2	Q30366	Q30366 streptococc
874	6	3.4	228	2	Q29279	Q29279 archaeoglob	947	6	3.4	245	2	Q8P0G8	Q8P0g8 bruceella me
875	6	3.4	228	2	Q7QDM6	Q7qdm6 anopheles g	948	6	3.4	245	2	Q8YEL9	Q8Yel9 bruceella me
876	6	3.4	228	2	Q679I2	Q679i2 mirounga an	949	6	3.4	245	2	Q8G364	Q8G364 rhizobium m
877	6	3.4	229	2	Q7QAY5	Q7qay5 anopheles g	950	6	3.4	245	2	Q9KCT0	Q9Kct0 agrobacteri
878	6	3.4	229	2	Q8DSQ2	Q8dsq2 streptococc	951	6	3.4	245	2	Q8UGB3	Q8Ugb3 agrobacteri
879	6	3.4	229	2	Q8FBL7	Q8fbl7 escherichia	952	6	3.4	245	2	Q8UIY1	Q8Uiy1 azospirillum
880	6	3.4	229	2	Q91W91	Q91w91 mus musculu	953	6	3.4	246	1	NODG_AZOB	NODG_AZOB
881	6	3.4	230	1	RECK_AGRTS	Q8u8r2 agrobacteri	954	6	3.4	246	2	Q9N4A0	Q9N4A0 caenorhabdi
882	6	3.4	230	2	Q6ICJ4	Q6icj4 homo sapien	955	6	3.4	246	2	Q9U4U4	Q9U4u4 cryptospori
883	6	3.4	230	2	Q6JHR1	Q6jhr1 saccharopol	956	6	3.4	246	2	Q7W4I5	Q7W4i5 bordetella
884	6	3.4	230	2	Q7MH80	Q7mh80 vibrio vuln	957	6	3.4	246	2	Q7W0N2	Q7W0n2 streptomyce
885	6	3.4	230	2	Q7NJJ0	Q7njj0 gloeobacter	958	6	3.4	246	2	Q8A2I2	Q8A2i2 vibrio vuln
886	6	3.4	231	2	Q86OK1	Q86ok1 adineta vag	959	6	3.4	246	2	Q8DA72	Q8DA72 shigella bo
887	6	3.4	231	2	Q93W48	Q93w48 bacillus th	960	6	3.4	247	2	Q6O0X0	Q6O0x0 manihelma
888	6	3.4	231	2	Q89E35	Q89e35 bradyrhizob	961	6	3.4	247	2	Q65U71	Q65u71 rhizobium e
889	6	3.4	232	2	Q6YWY3	Q6ywy3 oryza sativ	962	6	3.4	249	2	Q8KL79	Q8KL79
890	6	3.4	232	2	Q8PMW2	Q8pmw2 xanthomonas	963	6	3.4	250	1	WSE2_HUMAN	WSE2_HUMAN
891	6	3.4	233	1	RPE_CHLTR	Q84123 chlamydia t	964	6	3.4	250	1	Y0E2_PROLL	Y0E2_PROLL
892	6	3.4	233	2	Q81X39	Q81x39 cloning vec	965	6	3.4	250	2	Q9P9C3	Q9P9c3 uncultured
893	6	3.4	233	2	Q7MX39	Q7mx39 homo sapien	966	6	3.4	250	2	Q17154	Q17154 caenorhabdi
894	6	3.4	233	2	Q7W6H4	Q7w6h4 wolinnella s	967	6	3.4	250	2	Q6B355	Q6B355 uncultured
895	6	3.4	233	2	Q893J4	Q893j4 clostridium	968	6	3.4	250	2	Q9KKK5	Q9KKk5 corynebacte
896	6	3.4	234	2	Q7NZN8	Q7nzn8 chromobacte	969	6	3.4	250	2	Q81174	Q81174 bacillus ce
897	6	3.4	234	2	Q82MP8	Q82mp8 streptomyce	970	6	3.4	250	2	Q6AL91	Q6Al91 bradyrhizob
898	6	3.4	234	2	Q82SP8	Q82sp8 nitrosomona	971	6	3.4	250	2	Q6AL91	Q6Al91 desulfotale
899	6	3.4	234	2	Q8EMT5	Q8emt5 mycoplasma	972	6	3.4	251	2	Q6HC40	Q6Hc40 bacillus th
900	6	3.4	235	2	Q817B9	Q817b9 echinococcu	973	6	3.4	251	2	Q8S2R9	Q8S2r9 theilungiel
901	6	3.4	235	2	Q8R0A6	Q8r0a6 mus musculu	974	6	3.4	251	2	Q8R4A6	Q8R4a6 xanthomonaer
902	6	3.4	235	2	Q921F5	Q921f5 mus musculu	975	6	3.4	252	2	Q9FH68	Q9FH68 arabidopsis
903	6	3.4	235	2	Q6GLA0	Q6glao xenopus tro	976	6	3.4	252	2	Q6LTC3	Q6Ltc3 photobacter
904	6	3.4	236	2	Q7RNS7	Q7rns7 plasmodium	977	6	3.4	252	2	Q7TUI1	Q7Tui1 rhodospirell
905	6	3.4	236	2	Q9VZ10	Q9vz10 drosophilla	978	6	3.4	252	2	Q9XK25	Q9Xk25 bacillus ha
906	6	3.4	236	2	Q8Y4B5	Q8y4b5 listeria mo	979	6	3.4	252	2	Q9KRM9	Q9Krm9 bacillus ha
907	6	3.4	236	2	Q927Z2	Q927z2 listeria in	980	6	3.4	252	2		

981 6 3.4 253 2 Q6CFY6 Q6CFY6 yarrowia 11  
 982 6 3.4 253 2 Q6F9R6 Q6F9R6 actinobact  
 983 6 3.4 253 2 Q89CF1 Q89CF1 bradyrhizob  
 984 6 3.4 254 2 Q8NDT5 Q8NDT5 homo sapien  
 985 6 3.4 254 2 Q95XU1 Q95XU1 caenorhabdi  
 986 6 3.4 254 2 Q9V3R0 Q9V3R0 dirosophila  
 987 6 3.4 254 2 Q632B0 Q632B0 bacillus ce  
 988 6 3.4 254 2 Q72YCS Q72YCS bacillus ce  
 989 6 3.4 254 2 Q816A9 Q816A9 bacillus ce  
 990 6 3.4 254 2 Q81XP1 Q81XP1 bacillus an  
 991 6 3.4 254 2 Q6HB08 Q6HB08 bacillus th  
 992 6 3.4 254 2 Q8QNB1 Q8QNB1 ectocarpus  
 993 6 3.4 255 2 Q81BQ1 Q81BQ1 plasmodium  
 994 6 3.4 255 2 Q8RL62 Q8RL62 pseudomonas  
 995 6 3.4 255 2 Q929Y8 Q929Y8 actinobacil  
 996 6 3.4 255 2 Q8BCX9 Q8BCX9 xanthomonas  
 997 6 3.4 255 2 Q8PPB7 Q8PPB7 xanthomonas  
 998 6 3.4 255 2 Q61QH2 Q61QH2 brachydanio  
 999 6 3.4 256 2 Q81TL5 Q81TL5 mechanosarc  
 1000 6 3.4 256 2 Q8ZRR8 Q8ZRR8 salmonella

## ALIGNMENTS

RESULT 1  
 IL20\_HUMAN STANDARD; PRT; 176 AA.  
 ID Q9NYT1; Q96QZ6; 28-FEB-2003 (Rel. 41, Created)  
 AC Q9NYT1; Q96QZ6; 28-FEB-2003 (Rel. 41, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10)  
 DE (UN085/PRO1801).  
 GN Name=IL20;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2109717; PubMed=11163336; DOI=10.1016/S0092-8674(01)00187-8;  
 RA Blumberg P., Conklin D., Xu W.F., Grossmann A., Brendler T.,  
 RA Carillo S., Ragan M., Foster D., Haldeman B.A., Hammond A., Haugen H.,  
 RA Jellinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,  
 RA Prunkard D., Saxon S., Sprecher C., Maggiora K., West J.,  
 RA Whitmore T.S., Yao L., Kuechle M.K., Dale B.A., Chandrasekhar Y.A.;  
 RA "Interleukin 20: discovery, receptor identification, and role in  
 RA "interleukin function.";  
 RA Cell 104:9-19(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Adaya B., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Helms S.,  
 RA Huang A., Kim H.S., Klimowksi L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,  
 RA Seisagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vanden R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yamasura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;  
 RA "The secreted protein discovery initiative (SPDI), a large-scale  
 RA effort to identify novel human secreted and transmembrane proteins: a  
 RA bioinformatics assessment.";  
 RA Genome Res. 13:2265-2270(2003).

RN [4]  
 RP SEQUENCE OF 25-39.  
 RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 CC -1- FUNCTION: Cytokine that may be involved in epidermal function and  
 CC peristalsis. Acts through SPAT3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed at very low levels in skin, trachea,  
 CC and other tissues.  
 CC -1- SIMILARITY: Belongs to the IL-10 family.  
 CC -----  
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DR EMBL; AF224266; AAF36679.1; -;  
 DR EMBL; AF402002; AAK84423.1; -;  
 DR EMBL; AY358320; AAQ86866.1; -;  
 DR HSSP; Q9UHD0; INF.  
 DR GenSeq; HGNC:6002; IL20.  
 DR MIM; 605619; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0045517; F:interleukin-20 receptor binding; TAS.  
 DR GO; GO:0045606; P:positive regulation of epidermal cell diffe. . . ; TAS.  
 DR GO; GO:0045618; P:positive regulation of keratinocyte diffe. . . ; TAS.  
 DR GO; GO:0042517; P:positive regulation of tyrosine phosphoryla. . . ; TAS.  
 DR GO; GO:0050727; P:regulation of inflammatory response; TAS.  
 DR InterPro; IPR000098; Interleukin\_10.  
 DR ProDom; PD003687; Interleukin\_10; 1.  
 DR PROSITE; PS00520; INTERLEUKIN\_10; 1.  
 DR KW Cytokine; Direct protein sequencing; signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 176 Interleukin-20.  
 FT DISULFID 33 126 Potential.  
 FT DISULFID 80 132 Potential.  
 FT DISULFID 81 134 Potential.  
 FT CONFLICT 48 48 E -> D (in Ref. 1).  
 FT CONFLICT 126 126 C -> S (in Ref. 3).  
 SQ SEQUENCE 176 AA; 20072 MM; 83859925086C447 CNG64;  
 Query Match 72.7%; Score 128; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-125;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 49 IRGSOAKDGNIDIRILRTSTLDTKPRANCCILRLRLYLDRVFNQYOTPHYTLRK 108  
 DB 49 IRGSOAKDGNIDIRILRTSTLDTKPRANCCILRLRLYLDRVFNQYOTPHYTLRK 108  
 QY 109 ISSIANSFLITTKDRLCHAMTCHCGEANKKTSQILSHFEKLEPQAAYKALGELDIL 168  
 DB 109 ISSIANSFLITTKDRLCHAMTCHCGEANKKTSQILSHFEKLEPQAAYKALGELDIL 168  
 QY 169 LQNMETE 176  
 DB 169 LQNMETE 176  
 RESULT 2  
 IL20\_MOUSE STANDARD; PRT; 176 AA.  
 ID Q9JUV9;  
 AC Q9JUV9; 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-20 precursor (IL-20) (Four alpha helix cytokine ZCYTO10).  
 GN Name=IL20;

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=21097717; PubMed=11163336; DOI=10.1016/S0092-8674(01)00187-8;
RA Blumberg H., Conklin D., Xu W.F., Grossmann A., Brander T.,
RA Carillo S., Egan M., Foster D., Haldeman B.A., Hammond H.,
RA Jelinek L., Kelly J.D., Madden K., Maurer M.F., Parrish-Novak J.,
RA Prunkard D., Sexson S., Sprecher C., Maggie K., West J.,
RA Whitmore T.E., Yao L., Knechle M.K., Dale B.A., Chandrasekhar V.A.;
RT "Interleukin 20: discovery, receptor identification, and role in
RT epidermal function.";
RL Cell 104:9-19(2001).
CC -1- FUNCTION: Cytokine that may be involved in epidermal function and
CC psoriasis. Acts through STAT3.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-10 family.
CC -----
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CC -----
DR EMBL; AF224267; AAF36680.1; -.
DR HSSP; Q9UHD0; INIF.
DR MGD; MGI:1890473; IL20.
DR GO; GO:0045517; P:interleukin-20 receptor binding; IPI.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000098; Interleukin_10.
DR ProDom; PD003687; Interleukin_10; 1.
DR SMART; SM00188; IL10; 1.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR DR Cytokine; Signal.
KW SIGNAL.
FT CHAIN 1 24 Potential.
FT DISULFID 25 176 Interleukin-20.
FT DISULFID 33 126 Potential.
FT DISULFID 80 132 Potential.
FT DISULFID 81 134 Potential.
SQ SEQUENCE 176 AA; 20097 MW; 08577AF65657771 CRC64;

Query Match 7.4%; Score 13; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 TLTKISSIANSFL 117
DB 105 TLTKISSIANSFL 117

RESULT 3
O6L2K4 PRELIMINARY; PRT; 137 AA.
AC O6L2K4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical membrane spanning protein.
GN OrderedLocuNames=PT00213;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fletterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,

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RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AB017261; AAT42798.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 16535 MW; DD2928CD82E98D01 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ISAFYTL 18
DB 46 ISAFYTL 53

RESULT 4
SURE_PSEPK STANDARD; PRT; 249 AA.
ID SURE_PSEPK
AC Q8BMF1;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid phosphatase sure (EC 3.1.3.2).
GN Name=sure; OrderedLocuNames=PP1620;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beaman M.C., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouf H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzez A., Utechtack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Medler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Helm S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmiller B.,
RA Praser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
CC -1- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
CC phosphate.
CC -1- Cofactor: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the sure acid phosphatase family.
CC -----
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CC -----
DR EMBL; AB016780; AAM67241.1; -.
DR HSSP; P96112; IJ9L.
DR TIGR; PP1620; -.
DR HAMAP; MF_00060; -1.
DR InterPro; IPR002828; SURE.
DR Pfam; PF01975; SURE; 1.
DR ProDom; PD005378; SURE; 1.
KW Complete proteome; Hydrolyase; Magnesium.
FT ACT_SITE 123 123 Potential.
FT METAL 8 8 Magnesium (By similarity).
FT METAL 9 9 Magnesium (By similarity).
FT METAL 39 39 Magnesium (By similarity).
FT METAL 91 91 Magnesium (By similarity).
SQ SEQUENCE 249 AA; 26317 MW; 824P1D5E7C8B8073 CRC64;

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Query Match 4.5%; Score 8; DB 1; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLAFSLLS 12  
 |||||  
 DB 119 SLAFSLLS 126

## RESULT 5

ID Q9KDB7 PRELIMINARY; PRT; 279 AA.  
 AC Q9KDB7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE BH1296 protein.  
 GN OrderedLocustNames=BH1296;  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125;  
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;  
 RA Takami H., Nakasone K., Takeki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.,  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.",  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL, AP001511; BAB05015.1; -.  
 DR PIR; H63811; H63811.  
 KW Complete proteome.  
 SQ SEQUENCE 279 AA; 32457 MM; D92AE286356C30D5 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFSLLSA 13  
 |||||  
 DB 13 LAFSLLSA 20

## RESULT 6

ID Q8UIB8 PRELIMINARY; PRT; 305 AA.  
 AC Q8UIB8; Q7D1K4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein Atu0379 (AGR\_C\_664p).  
 GN OrderedLocustNames=AGR\_C\_664; Atu0379;  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Dupont;  
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;  
 RA Wood D.W., Seubai J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,  
 RA Chapman P., Leventy R., Li M.-J., McClelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RT Science 294:2317-2323(2001).  
 RL [2]  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Cereoni;  
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Hailing C., Mullin L.,  
 RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,  
 RA William C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
 RA Fiejo C., Slater S.,  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL, AE009009; AAL41401.1; -.  
 DR EMBL, AE007975; AAK6196.1; -.  
 DR PIR; C97405; C97405.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 305 AA; 32574 MM; A2A4683FD67AEFF0 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 QAAVVKAL 162  
 |||||  
 DB 256 QAAVVKAL 263

## RESULT 7

ID Q82S35 PRELIMINARY; PRT; 396 AA.  
 AC Q82S35;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Restriction modification system, type I (BC 3.1.21.3).  
 GN OrderedLocustNames=NE2526;  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RX DOI=10.1128/JB.185.9.2759-2773.2003;  
 RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
 RA Archiero D.M., Hommes N.G., Whitaker M.M., Arp D.J.,  
 RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea.";  
 RL J. Bacteriol. 185:2759-2773(2003).  
 DR EMBL; BX321865; CAD86438.1; -.  
 DR GO; GO:0003677; P:DNA binding; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0009035; F:type I site-specific deoxyribonuclease actl. .; IEA.  
 DR GO; GO:0006304; P:DNA modification; IEA.  
 DR InterPro; IPR000055; Rest. mod. DNA.  
 DR Pfam; PF01420; Methylase S; 2.  
 KW Complete proteome; Hydrolyase.  
 SQ SEQUENCE 396 AA; 43995 MM; 056FC6AB5DCA9DC CRC64;

Query Match 4.5%; Score 8; DB 2; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 SSLANSFL 117  
 |||||  
 DB 198 SSLANSFL 205

```

RESULT 8
ANSP_STRCO
ID ANSP_STRCO STANDARD; PRT; 489 AA.
AC Q9X7P0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE L-asparagine permease (L-asparagine transport protein).
GN Name:ansp; OrderedLocustNames=SC06734; ORNames=SC5F2A.17;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_Taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12009553; DOI=10.1038/41741a1;
RX Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Godle A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Laire L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)".
RT Nature 417:141-147(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the amino acid-polyamine-organocation (APC)
CC superfamily. Amino acid transporter (AAT) (TC 2.A.3.1) family.
CC -----
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CC -----
DR DR EMBL: AL939129; CAB40684.1; -.
DR PIR: T35259; T35259.
DR InterPro: IPR002293; AA/permease1.
DR InterPro: IPR004840; AAC_permease.
DR InterPro: IPR004841; Permease_region.
DR Pfam: PF00324; AA_permease; 1.
DR TIGRfam: TIGR01773; GABAperme; 1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
KW Amino-acid transport; Complete proteome; Transmembrane; Transport.
KW -----
FT TRANSMEM 38 58 Potential.
FT TRANSMEM 62 82 Potential.
FT TRANSMEM 113 133 Potential.
FT TRANSMEM 150 170 Potential.
FT TRANSMEM 175 195 Potential.
FT TRANSMEM 223 243 Potential.
FT TRANSMEM 268 288 Potential.
FT TRANSMEM 302 322 Potential.
FT TRANSMEM 357 377 Potential.
FT TRANSMEM 382 402 Potential.
FT TRANSMEM 426 446 Potential.
FT TRANSMEM 452 472 Potential.
SQ SEQUENCE 489 AA; 51797 MW; 219F74312E81F14C CRC64;

Query Match 4.5%; Score 8; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 158 VVKALGEL 165
DB 81 VVKALGEL 88

```

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RESULT 9
MURE_BIFLO
ID MURE_BIFLO STANDARD; PRT; 517 AA.
AC O8G4M3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-N-acetylmutaroyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase
DB (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNac-tripeptide synthetase).
GN Name=mure; OrderedLocustNames=BL1356;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteriales; Actinomycetales; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_Taxid=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RC MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RX Schell M.A., Karmirantzou M., Snell B., Villanova D., Berger B.,
RA Pessi G., Zwaan M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RT Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminopimelate = ADP + phosphate + UDP-
CC N-acetylmuramoyl-L-alanyl-D-glutamate + meso-2,6-diamino-
CC heptanedioate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the murCDSF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL: AE014765; AAN25156.1; -.
DR HAMAP: MF_00208; -.
DR InterPro: IPR004101; Mur_Ligase_C.
DR InterPro: IPR000713; Mur_Ligase_N.
DR Pfam: PF01225; Mur_Ligase; 1.
DR Pfam: PF02875; Mur_Ligase_C; 1.
KW ATP-binding; Cell division; Cell wall; Complete proteome; Ligase;
KW Peptidoglycan synthesis.
KW -----
FT NP_BIND 125 131s ATP (Potential).
SQ SEQUENCE 517 AA; 56338 MW; 87F39226FD059A0F CRC64;

Query Match 4.5%; Score 8; DB 1; Length 517;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 9 SLISAAFY 16
DB 104 SLISAAFY 111

RESULT 10
Q7ZVGO
ID Q7ZVGO PRELIMINARY; PRT; 531 AA.
AC Q7ZVGO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Regulator of chromosome condensation (RCC1) and BTB (POZ) domain

```

DE containing protein 1.  
 GN ORFNames=zgc:56037;  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 CC Cyprinidae; Danio.  
 OK NCBI\_TaxID=7955;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RX MEDLINE=22288557; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausberg R.D., Collins F.S., Wagner I., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buelew K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blackley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AB; TISSUE=whole body;  
 RA Strusberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC045877; AAH45877.1; -.  
 DR HSSP; O87916; IJTD.  
 DR ZFIN; ZDB-GENE-030131-7951; zgc:56037.  
 DR GO; GO:0005515; P:protein binding; IEA.  
 DR InterPro; IPR000210; BTB\_PZ.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR009091; RCCT/BLIP-II.  
 DR InterPro; IPR00408; Reg\_chc\_condens.  
 DR Pfam; PF00651; BTB; 2.  
 DR PRINTS; PR00633; RCNDNSATION.  
 DR SMART; SM00225; BTB; 1.  
 DR PROSITE; PS50097; BTB; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00626; RCCT\_2; 2.  
 DR PROSITE; PS50012; RCCT\_3; 4.  
 DR SEQUENCE 531 AA; 58711 MW; D5D9C00ABB6A18D3 CRC64;  
 SO  
 Query Match 4.5%; Score 8; DB 2; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 AFSLSAA 14  
 Db 472 AFSLSAA 479  
 RESULT 11  
 Q83BA7 PRELIMINARY; PRT; 698 AA.  
 AC Q83BA7;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 GN Membrane protein, putative.  
 GN Ordered locus names=CBU1605;  
 OS Coxiella burnetii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;

OC Coxiellaceae; Coxiella.  
 OK NCBI\_TaxID=777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nine Mile phase I / RSA 493;  
 RX MEDLINE=2260857; PubMed=12704232; DOI=10.1073/pnas.0931379100;  
 RA Seeshadri R., Paulsen I.T., Eissen J.A., Read T.D., Nelson K.E.,  
 RA Nelson W.C., Ward N.L., Tetteilin H., Davidson T.M., Beaman M.J.,  
 RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,  
 RA Khouri H.M., Lee K.H., Carby H.A., Scanlan D., Heinzen R.A.,  
 RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;  
 RT "Complete genome sequence of the Q-fever pathogen, Coxiella  
 RT burnetii.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).  
 DR EMBL; AB016965; AAC91102.1; -.  
 DR TIGR; CBU1605; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR01066; Mscs\_channel\_C.  
 DR InterPro; IPR006885; Mscs\_channel.  
 DR InterPro; IPR01014; Mscs\_transmembr.  
 DR InterPro; IPR010920; Sm\_like\_riboprot.  
 DR Pfam; PF00924; Msc\_channel; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 698 AA; 79951 MW; 3A5251E0A7FFDB5E CRC64;  
 SO  
 Query Match 4.5%; Score 8; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 SLSAFLSL 11  
 Db 650 SLSAFLSL 657  
 RESULT 12  
 P5CS\_LYCSES STANDARD; PRT; 717 AA.  
 AC 096480;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Delta 1-pyrroline-5-carboxylate synthetase (P5CS) [Includes: Glutamate  
 DE 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK); Gamma-glutamyl  
 DE phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde  
 DE dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)].  
 GN Name=PRO2;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 CC Lamiales; Solanales; Solanaceae; Solanum.  
 OK NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Alisa Craig;  
 RA Magglio A., Garcia-Rios M., Fujita T., Bressan R.A., Joly R.J.,  
 RA Hasegawa M.P., Geonka L.N.;  
 RT "Cloning of tomato and tomato2 from Lycopersicon esculentum L.:  
 RT coexistence of polyclonal and monoclonal genes which encode the  
 RT enzymes catalyzing the first two steps of proline biosynthesis.";  
 RL (ex) Plant Gene Register PGR96-077.  
 CC -1- FUNCTION: P5CS plays a key role in proline biosynthesis, leading  
 CC to osmoregulation in plants.  
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate = ADP + L-glutamate 5-  
 CC phosphate.  
 CC -1- CATALYTIC ACTIVITY: L-glutamate 5-semialdehyde + phosphate +  
 CC NADP(+) = L-glutamyl 5-phosphate + NADPH.  
 CC -1- ENZYME REGULATION: Feedback regulated by proline.  
 CC -1- PATHWAY: Proline biosynthesis; first step.  
 CC -1- PATHWAY: Proline biosynthesis; second step.  
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in leaves and is  
 CC inducible in roots subjected to salt stress.  
 CC -1- SIMILARITY: In the N-terminal section; belongs to the glutamate 5-  
 CC kinase family.

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CC -1- SIMILARITY: In the C-terminal section; belongs to the gamma-
CC glutamyl phosphate reductase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U60267, AAB67875.1; -.
CC PIR: T07422, T07422.
CC HSSP: Q9WC9, 1020.
CC InterPro: IPR001048; Aa_kinase.
CC InterPro: IPR000965; Gg_lut_pp_reduct.
CC InterPro: IPR001057; Glu_5_kinase.
CC InterPro: IPR005766; P5_carboxy_syn.
CC InterPro: IPR005715; Prob.
CC Pfam: PF00696; Aa_kinase; 1.
CC PRINTS: PR00474; GLUSKINASE.
CC TIGRfam: TIGR01092; P5CS; 1.
CC TIGRfam: TIGR00407; ProA; 1.
CC PROSITE: PS00902; GLUTAMATE_5_KINASE; 1.
CC PROSITE: PS01223; PROA; 1.
CC Kinase; Multifunctional enzyme; NADP; Oxidoreductase;
CC Proline biosynthesis; Transferase.
CC DOMAIN 1 296 Glutamate 5-kinase.
CC FT DOMAIN 1 296 Gamma-glutamyl phosphate reductase.
CC SQ SEQUENCE 717 AA; 77589 MW; 1E206428B69EEBCA CRC64;

Query Match 4.5%; Score 8; DB 1; Length 717;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 KISSLANS 115
Db 365 KISSLANS 372

RESULT 13
Q7MBR3 PRELIMINARY; PRT; 719 AA.
AC Q7MBR3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative toxin secretion ABC transporter, ATP-binding subunit.
GN OrderedocusNames=VVA1677;
OS Vibrio vulnificus (strain V016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=196600;
OX [1]
RP SEQUENCE FROM N.A.
RX PubMed=14655695; DOI=10.1101/gr.1295503;
RA Chen C.-T., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Shao T.-L., Liu Y.-M., Chen H.-D., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Liao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587(2003).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC EMBL: AP005351, BAC97703.1; -.
CC HSSP: P26361, 1R0W.
CC GO: GO:0016021; C: integral to membrane; IEA.
CC GO: GO:0005524; F: ATP binding; IEA.
CC GO: GO:0042626; F: ATPase activity; IEA.
CC GO: GO:0008223; F: peptidase activity; IEA.
CC GO: GO:0006508; P: proteolysis and peptidolysis; IEA.
CC GO: GO:0006810; P: transport; IEA.
CC InterPro: IPR011527; ABC_membrane_1.

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DR InterPro: IPR001140; ABC_TM_transp.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR005074; Peptidase_C39.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF03412; Peptidase_C39; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR PROSITE: PS50929; ABC_TM1F; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
DR ATP-binding; Complete proteome.
SQ SEQUENCE 719 AA; 80876 MW; 6144A6D1EC0505A7 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LRRHLRL 89
Db 258 LRRHLRL 265

RESULT 14
Q8E874 PRELIMINARY; PRT; 725 AA.
AC Q8E874;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Toxin secretion ABC transporter, ATP-binding subunit/permease protein,
DE putative.
GN OrderedocusNames=SOA0049;
OS Shewanella oneidensis.
OG Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NR-1;
RC MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Galois B.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Melhe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Dukin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impram M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouli H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nelson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC EMBL: A015912; AAN5285.1; -.
CC HSSP: P08716, 1MT0.
CC MEROPS: C39.005; -.
CC TIGR: SOA0049; -.
CC GO: GO:0016021; C: integral to membrane; IEA.
CC GO: GO:0005524; F: ATP binding; IEA.
CC GO: GO:0042626; F: ATPase activity; IEA.
CC GO: GO:0000166; F: nucleotide binding; IEA.
CC GO: GO:0008233; F: peptidase activity; IEA.
CC GO: GO:0006508; P: proteolysis and peptidolysis; IEA.
CC InterPro: IPR003593; AAA_ATPase.
CC InterPro: IPR011527; ABC_membrane_1.
CC InterPro: IPR001140; ABC_TM_transp.
CC InterPro: IPR003439; ABC_transporter.
CC InterPro: IPR005074; Peptidase_C39.
CC Pfam: PF00664; ABC_membrane; 1.
CC Pfam: PF00005; ABC_tran; 1.
CC Pfam: PF03412; Peptidase_C39; 1.
CC ProDom: PD000006; ABC_transporter; 1.

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DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS50929; ABC\_TM1F; 1.  
 DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 725 AA; 80452 MW; 890B16CE3A6639B2 CRC64;

Query Match 4.5%; Score 8; DB 2; Length 725;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LRRLLRL 89  
 |||||  
 Db 263 LRRLLRL 270

## RESULT 15

Q9XGC4 PRELIMINARY; PRT; 762 AA.  
 AC Q9XGC4;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Pyroline-5-carboxylate synthetase (EC 2.7.2.11).  
 GN Name=p5c8;  
 OS Vitis vinifera (Grape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Vitaceae; Vitis.  
 OC NCBI\_TaxID=29760;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Grape berry;  
 RX MEDLINE=99329329; PubMed=10398729; DOI=10.1104/pp.120.3.923;  
 RT "Stines A.P., Naylor D.J., Hoj P.H., van Heeswijk R.;  
 RT "Proline accumulation in developing grapevine fruit occurs  
 RT independently of changes in the levels of delta1-pyroline-5-  
 RT carboxylate synthetase mRNA or protein."  
 RL Plant Physiol. 120:923-923 (1999).  
 DR EMBL; AJ005686; CAB40834.1; -.  
 DR HSR; Q9WYC9; 1020.  
 DR GO; GO:0005737; Cytoplasm; IEA.  
 DR GO; GO:0004349; F:glutamate 5-kinase activity; IEA.  
 DR GO; GO:0004350; F:glutamate-5-semialdehyde dehydrogenase acti. .; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0008652; P:amino acid biosynthesis; IEA.  
 DR GO; GO:000561; P:proline biosynthesis; IEA.  
 DR InterPro; IPR001048; Aa\_Kinase.  
 DR InterPro; IPR000965; Glnut\_PP\_reduct.  
 DR InterPro; IPR001057; Gln 5Kinase.  
 DR InterPro; IPR005715; P5\_Carboxy\_syn.  
 DR Pfam; PF00696; Aa\_Kinase; 1.  
 DR PRINTS; PIRSF036429; P5C\_syn; 1.  
 DR PRINTS; PRO0474; Gln5KINASE.  
 DR TIGRfams; TIGR01092; P5CS; 1.  
 DR TIGRfams; TIGR00407; p5c8; 1.  
 DR TIGRfams; TIGR01027; p5c8; 1.  
 KW transferase.  
 SQ SEQUENCE 762 AA; 82682 MW; 586A3A48FC8A1C CRC64;

Query Match 4.5%; Score 8; DB 2; Length 762;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 KISSLANS 115  
 |||||  
 Db 367 KISSLANS 374

Search completed: November 2, 2005, 19:01:38  
 Job time : 236 secs



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OM protein - protein search, using sw model

Run on: November 2, 2005, 18:51:12 / Search time 39 Seconds  
(without alignments)  
434.209 Million cell updates/sec

Title: US-10-748-484-2  
Perfect score: 176  
Sequence: 1 MKASLSAPLSAPAFYLLMT.....AVKALGLDILLQNMETE 176

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 860

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	4.5	279	2	H83811	hypothetical prote
2	4.5	305	2	AC2623	conserved hypochet
3	4.5	305	2	C97405	hypothetical prote
4	4.5	489	2	T35259	probable L-asparag
5	4.5	717	2	T07422	delta 1-pyrroline-
6	4.0	201	2	A47096	response regulator
7	4.0	213	2	G84828	hypothetical prote
8	4.0	217	2	JC5710	TBP-1 interacting
9	4.0	224	2	G70851	probable gid prote
10	4.0	241	2	C75329	conserved hypochet
11	4.0	251	2	T24485	hypothetical prote
12	4.0	260	2	T32329	hypothetical prote
13	4.0	293	2	E71674	hypothetical prote
14	4.0	327	2	A70392	UDP-glucose-4-epim
15	4.0	354	2	T04262	mitogen-activated
16	4.0	382	2	S63638	ubiquinol-cytochro
17	4.0	388	2	A47032	galactokinase galk
18	4.0	389	2	S36638	glycoprotein Epi -
19	4.0	426	1	B69656	multidrug-efflux t
20	4.0	441	2	F71482	hypothetical prote
21	4.0	444	2	F96838	hypothetical prote
22	4.0	445	2	B86160	F22D16.4 protein -
23	4.0	471	2	T19147	probable protein k
24	4.0	473	2	T41500	hypothetical prote
25	4.0	478	2	C95981	probable membrane
26	4.0	480	2	T00971	NAD(P) transhydrog
27	4.0	512	2	D82444	probable transport
28	4.0	628	2	T38034	ATP synthase, chain
29	4.0	649	2	C81687	

30	7	4.0	706	2	P86143
31	7	4.0	754	2	T00393
32	7	4.0	761	2	T05299
33	7	4.0	762	2	E64597
34	7	4.0	762	2	H71916
35	7	4.0	915	2	H96709
36	7	4.0	930	2	AG0410
37	7	4.0	1100	2	T47940
38	7	4.0	2165	2	T21371
39	7	4.0	4563	1	LPHUB
40	7	3.4	54	2	H31445
41	6	3.4	54	2	F61494
42	6	3.4	54	2	F31447
43	6	3.4	55	2	AP2035
44	6	3.4	56	2	AP6837
45	6	3.4	62	2	D59103
46	6	3.4	63	2	S00951
47	6	3.4	66	2	D72607
48	6	3.4	69	2	F90476
49	6	3.4	70	2	AH1043
50	6	3.4	71	2	AI0691
51	6	3.4	71	2	B85769
52	6	3.4	71	2	C64919
53	6	3.4	71	2	F90920
54	6	3.4	71	2	F81897
55	6	3.4	71	2	B63337
56	6	3.4	76	2	D81094
57	6	3.4	76	2	S74780
58	6	3.4	76	2	AG2612
59	6	3.4	80	2	B38908
60	6	3.4	81	2	C49029
61	6	3.4	81	2	T03707
62	6	3.4	84	2	T11970
63	6	3.4	86	2	AB0153
64	6	3.4	88	2	A90048
65	6	3.4	89	2	I51423
66	6	3.4	89	2	AP3590
67	6	3.4	92	2	S36498
68	6	3.4	92	2	T03665
69	6	3.4	92	2	T03617
70	6	3.4	95	2	I46684
71	6	3.4	100	2	F84766
72	6	3.4	114	2	E97638
73	6	3.4	114	2	AF2861
74	6	3.4	115	2	H83430
75	6	3.4	117	2	E72732
76	6	3.4	117	2	A82495
77	6	3.4	118	2	AG2077
78	6	3.4	118	2	H72644
79	6	3.4	122	2	B86570
80	6	3.4	122	2	G72054
81	6	3.4	122	2	E81664
82	6	3.4	122	2	D42645
83	6	3.4	122	2	C64422
84	6	3.4	123	2	A83432
85	6	3.4	124	2	S45788
86	6	3.4	126	2	B82690
87	6	3.4	127	2	A97056
88	6	3.4	127	2	B89862
89	6	3.4	127	2	AD2636
90	6	3.4	127	2	C84502
91	6	3.4	129	2	F70670
92	6	3.4	133	2	A72675
93	6	3.4	139	2	A70881
94	6	3.4	141	2	F38164
95	6	3.4	141	2	A83178
96	6	3.4	141	2	F69392
97	6	3.4	141	2	G72661
98	6	3.4	142	1	HAGY
99	6	3.4	143	2	H71970
100	6	3.4	145	2	AE2962
101	6	3.4	145	2	E88462
102	6	3.4	151	2	A96493

hypothetical prote
Nitrogen breakage
hypothetical prote
DNA mismatch repai
hypothetical prote
two-component regu
hypothetical prote
hypothetical prote
apolipoprotein B-1
ovomucoid, chird d
ovomucoid (PSTI-cy
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hemoglobin alpha c
conserved hypochet
protein C05H8.2 [1
hypothetical prote

103	6	3.4	152	2	D97462	hypothetical prote	176	6	3.4	226	2	C69760	amino acid ABC tra
104	6	3.4	152	2	AP2680	transcription regu	177	6	3.4	227	2	S41838	cytochrome-c oxida
105	6	3.4	153	2	B42748	trans-regulatory s	178	6	3.4	227	2	S26154	cytochrome-c oxida
106	6	3.4	153	2	G69426	riboflavin synthas	179	6	3.4	227	2	D81292	probable DNA methy
107	6	3.4	154	2	B87313	conserved hypothet	180	6	3.4	228	1	A44570	3-oxoadipate CoA-c
108	6	3.4	154	2	AF3354	translational initia	181	6	3.4	228	1	G69372	hypothetical prote
109	6	3.4	157	2	B64529	probable signal pe	182	6	3.4	230	2	B98234	hypothetical prote
110	6	3.4	158	2	T46080	hypothetical prote	183	6	3.4	233	2	B71553	probable ribulose-
111	6	3.4	159	1	MMYZN1	T3A protein - shae	184	6	3.4	236	2	AE1387	two-component resp
112	6	3.4	159	2	T06899	hypothetical prote	185	6	3.4	236	2	AG1762	two-component resp
113	6	3.4	159	2	AB2051	hypothetical prote	186	6	3.4	238	2	C70479	thiol-leuylidase in
114	6	3.4	160	2	S00714	phycocyanin 1 alph	187	6	3.4	239	2	C95323	conserved hypothet
115	6	3.4	160	2	AB3559	transcription regu	188	6	3.4	242	2	S49462	cyclin - rice
116	6	3.4	161	2	H96966	permease (imported	189	6	3.4	244	2	A56847	glutathione transf
117	6	3.4	162	2	S05712	phycocyanin 3 alph	190	6	3.4	245	2	D97493	3-oxoacyl-(acyl) ca
118	6	3.4	163	2	C71977	probable signal pe	191	6	3.4	245	2	AP2711	3-oxoacyl-(acyl) ca
119	6	3.4	164	2	T31280	benzoate 1,2-dioxy	192	6	3.4	245	2	AE3484	integral membrane
120	6	3.4	166	2	AB1150	transcription regu	193	6	3.4	245	2	F64465	hypothetical prote
121	6	3.4	166	2	AC1509	weakly transcrip	194	6	3.4	245	2	AB2596	transcription regu
122	6	3.4	167	1	RNGHD3	T-cell surface gly	195	6	3.4	245	2	D97378	histidine utilizat
123	6	3.4	168	2	C86241	protein T16B5.911	196	6	3.4	246	1	DRKNG	acetylacetyl-CoA re
124	6	3.4	168	2	T03168	hypothetical prote	197	6	3.4	252	2	P84047	3-oxoacyl-(acyl)-ca
125	6	3.4	172	2	H83634	conserved hypothet	198	6	3.4	252	2	B83706	hypothetical prote
126	6	3.4	173	1	RMMSD2	T-cell surface gly	199	6	3.4	258	2	G97163	flagellar basal bo
127	6	3.4	173	2	S37960	hypothetical prote	200	6	3.4	259	2	B82029	methionyl aminopep
128	6	3.4	174	2	F95921	glucose-1-phosphat	201	6	3.4	259	2	C81008	lysine-arginine-or
129	6	3.4	178	2	D82070	conserved hypothet	202	6	3.4	260	1	JKRCT	hypothetical prote
130	6	3.4	178	2	C71686	cytochrome c oxida	203	6	3.4	260	2	C65872	hypothetical prote
131	6	3.4	178	2	B83041	conserved hypothet	204	6	3.4	260	2	B91028	hypothetical prote
132	6	3.4	180	2	AP6321	hypothetical 15.0K	205	6	3.4	260	2	A69881	conserved hypothet
133	6	3.4	181	2	T35851	conserved hypothet	206	6	3.4	261	2	S55010	cytochrome-c oxida
134	6	3.4	182	2	A13074	conserved hypothet	207	6	3.4	261	2	H69976	hypothetical prote
135	6	3.4	183	2	H98211	hypothetical prote	208	6	3.4	261	2	D69606	spore coat-associat
136	6	3.4	183	2	T19276	hypothetical prote	209	6	3.4	261	2	S72895	hypothetical prote
137	6	3.4	183	2	H97760	hypothetical prote	210	6	3.4	261	2	AC0164	probable transport
138	6	3.4	184	2	S43486	B-cell maturation	211	6	3.4	262	1	OTFF3	cytochrome-c oxida
139	6	3.4	184	2	AC3051	conserved hypothet	212	6	3.4	262	1	OTFF3	cytochrome-c oxida
140	6	3.4	185	2	B64126	hypothetical prote	213	6	3.4	262	1	B64708	conserved hypothet
141	6	3.4	185	2	T13476	hypothetical prote	214	6	3.4	262	2	S69225	conserved hypothet
142	6	3.4	187	2	B83084	probable transcrip	215	6	3.4	263	2	G84021	naloxamycin polyke
143	6	3.4	188	2	H97750	cytochrome c oxida	216	6	3.4	265	2	F87668	D-beta-hydroxybuty
144	6	3.4	188	2	F69065	hypothetical prote	217	6	3.4	267	2	AB2362	hypothetical prote
145	6	3.4	189	2	C97476	hypothetical prote	218	6	3.4	267	2	H75429	transcription regu
146	6	3.4	191	2	S74158	CaMP-gated cation	219	6	3.4	268	2	S71200	agamous-like prote
147	6	3.4	192	2	A64242	glucose inhibited	220	6	3.4	268	2	C90321	hypothetical prote
148	6	3.4	192	2	S75403	hypothetical prote	221	6	3.4	268	2	D97054	probable membrane
149	6	3.4	193	2	H75508	sensory box protei	222	6	3.4	271	2	B71277	hypothetical prote
150	6	3.4	194	2	T45625	hypothetical prote	223	6	3.4	273	1	B75385	probable ribosomal
151	6	3.4	195	2	T46291	hypothetical prote	224	6	3.4	275	1	S38861	14-3-3 protein hom
152	6	3.4	196	2	I40130	outer surface prot	225	6	3.4	276	2	T29689	hypothetical prote
153	6	3.4	196	2	D83279	probable transcrip	226	6	3.4	277	1	PSAAB	epidermolitic toxi
154	6	3.4	197	1	WZVZCP	CF88 protein - shae	227	6	3.4	278	2	B99415	hypothetical prote
155	6	3.4	197	2	AB1230	B. subtilis ydei p	228	6	3.4	279	2	G83837	pyrroline-5-carbox
156	6	3.4	197	2	AE1583	B. subtilis ydei p	229	6	3.4	280	2	T32325	hypothetical prote
157	6	3.4	198	2	S61585	hypothetical prote	230	6	3.4	280	2	C82490	probable potassi
158	6	3.4	198	2	AE2379	hypothetical prote	231	6	3.4	282	2	S44825	F54F2.8 protein -
159	6	3.4	202	2	D81378	hypothetical prote	232	6	3.4	283	2	D72378	ribosomal protein
160	6	3.4	203	2	U01243	probable integral	233	6	3.4	283	2	S72343	sugar ABC transpor
161	6	3.4	203	2	A99865	coat protein 1 - b	234	6	3.4	283	2	T22618	opacity protein op
162	6	3.4	204	2	I38156	hypothetical prote	235	6	3.4	284	1	RSB871	hypothetical prote
163	6	3.4	204	2	H85753	rho protein GDP-di	236	6	3.4	286	1	T18957	site-specific reeo
164	6	3.4	204	2	B86308	partial probable p	237	6	3.4	287	2	S73992	hypothetical prote
165	6	3.4	206	2	S08632	P20D23.10 protein	238	6	3.4	287	2	B87194	probable peptidase
166	6	3.4	207	2	S21965	nodulin-21 - soybe	239	6	3.4	288	2	U01136	beta-lactamase (EC
167	6	3.4	210	2	T02928	prolactin - silver	240	6	3.4	288	2	T02327	nodulin-26 homolo
168	6	3.4	213	2	AC2379	physical impedance	241	6	3.4	292	2	G83332	probable transcrip
169	6	3.4	213	2	S54579	hypothetical prote	242	6	3.4	292	2	B88482	protein C05D11.9 f
170	6	3.4	214	4	S58320	hypothetical prote	243	6	3.4	293	2	S77254	phosphatidate cycl
171	6	3.4	220	2	B71811	hypothetical prote	244	6	3.4	293	2	G64592	hypothetical prote
172	6	3.4	224	2	T21896	hypothetical prote	245	6	3.4	294	2	AC2915	acetyl-CoA thioester
173	6	3.4	224	2	H97232	uncharacterized me	246	6	3.4	295	2	S35914	regulatory protein
174	6	3.4	224	2	AD1114	thiamin biosynthes	247	6	3.4	297	2	G90564	hypothetical prote
175	6	3.4	224	2	AE1475	thiamin biosynthes	248	6	3.4	297	2	H83058	hypothetical prote

249	6	3.4	297	2	ACT1494	322	6	3.4	340	2	S77165	hypothetical prote
250	6	3.4	297	2	A11135	323	6	3.4	341	2	C83067	hypothetical prote
251	6	3.4	298	2	T09921	324	6	3.4	342	2	T04054	protein kinase hom
252	6	3.4	298	2	B90550	325	6	3.4	342	2	T36505	probable ABC-type
253	6	3.4	298	2	B71317	326	6	3.4	343	2	H97057	transcription regu
254	6	3.4	299	2	D95412	327	6	3.4	343	2	D1873	grip 5'-region hea
255	6	3.4	300	1	H70557	328	6	3.4	343	2	H70517	probable lppd prot
256	6	3.4	300	2	F70605	329	6	3.4	343	2	B66468	probable DNA polym
257	6	3.4	300	2	AB1234	330	6	3.4	343	2	OXX12M	NADH2 dehydrogen
258	6	3.4	300	2	AC1597	331	6	3.4	346	2	C72353	hypothetical prote
259	6	3.4	300	2	D70510	332	6	3.4	347	2	T42528	Bcl1 protein homol
260	6	3.4	300	2	AE3088	333	6	3.4	347	2	T38998	probable galactosy
261	6	3.4	300	2	E96198	334	6	3.4	347	2	B69952	conserved hypotet
262	6	3.4	302	2	E72402	335	6	3.4	348	1	T26381	purple acid phosph
263	6	3.4	302	2	HE6823	336	6	3.4	349	2	E87284	sulfate-binding pr
264	6	3.4	302	2	AE1067	337	6	3.4	349	2	D84608	hypothetical prote
265	6	3.4	302	2	T38879	338	6	3.4	350	2	B87335	hypothetical prote
266	6	3.4	303	2	D83503	339	6	3.4	351	2	T42421	3-carboxy-cis,cis-
267	6	3.4	304	2	A49789	340	6	3.4	353	2	AF3114	ubiquinone biosynt
268	6	3.4	304	2	A35001	341	6	3.4	353	2	G98172	hypothetical prote
269	6	3.4	305	2	F95115	342	6	3.4	354	2	S28765	hypothetical prote
270	6	3.4	305	2	T52287	343	6	3.4	354	2	T31780	human microfibrill
271	6	3.4	305	2	A97158	344	6	3.4	355	2	T50093	hypothetical prote
272	6	3.4	306	2	D86805	345	6	3.4	355	2	S50372	coat protein VP2 -
273	6	3.4	306	2	AH2125	346	6	3.4	356	1	VVYP2L	hypothetical prote
274	6	3.4	306	2	T04879	347	6	3.4	356	2	E83591	protein gp20 (Bact
275	6	3.4	307	2	S56907	348	6	3.4	357	2	AC1360	lysophospholipase
276	6	3.4	307	2	P84502	349	6	3.4	358	2	B87464	conserved hypotet
277	6	3.4	308	2	B97002	350	6	3.4	358	2	G70026	hypothetical prote
278	6	3.4	309	2	T33612	351	6	3.4	358	2	AE2218	hypothetical prote
279	6	3.4	310	2	H75153	352	6	3.4	359	2	T47987	hypothetical prote
280	6	3.4	310	2	C75493	353	6	3.4	359	2	A86175	flagellar biosynth
281	6	3.4	311	2	B97985	354	6	3.4	360	2	AG2645	flnB protein (U951
282	6	3.4	311	2	A57223	355	6	3.4	360	2	G97427	mannose-1-phosphat
283	6	3.4	312	2	B75446	356	6	3.4	360	2	H81411	mannose-1-phosphat
284	6	3.4	313	2	E82123	357	6	3.4	361	2	T01007	conserved hypotet
285	6	3.4	313	2	I38176	358	6	3.4	361	2	H75260	G protein-coupled
286	6	3.4	313	2	I84474	359	6	3.4	361	2	H70422	GTP-binding protel
287	6	3.4	314	2	A75258	360	6	3.4	362	2	I65990	mannose-1-phosphat
288	6	3.4	315	2	D71525	361	6	3.4	362	2	D84952	conserved hypotet
289	6	3.4	315	2	A84634	362	6	3.4	362	2	T47698	hypothetical prote
290	6	3.4	316	2	P97689	363	6	3.4	365	2	T25309	hypothetical prote
291	6	3.4	316	2	D90585	364	6	3.4	365	2	T36004	probable PPB prote
292	6	3.4	316	2	G64408	365	6	3.4	368	2	G70802	hypothetical prote
293	6	3.4	317	2	D72050	366	6	3.4	368	2	A75166	opline catabolism h
294	6	3.4	318	2	D72050	367	6	3.4	369	2	A70019	transposase homolo
295	6	3.4	318	2	A86574	368	6	3.4	372	2	T44318	glycosyltransferas
296	6	3.4	319	2	T26450	369	6	3.4	372	2	I69647	ferriochrome ABC tr
297	6	3.4	320	2	S09208	370	6	3.4	373	2	H84404	ras-related GTPase
298	6	3.4	321	1	J00288	371	6	3.4	373	2	I38177	hypothetical prote
299	6	3.4	321	1	S58614	372	6	3.4	374	2	S48462	lps biosynthesis r
300	6	3.4	321	2	H86436	373	6	3.4	377	2	G75095	protein kinase (BC
301	6	3.4	323	2	C64087	374	6	3.4	377	1	OKXU1	hypothetical prote
302	6	3.4	324	2	A45752	375	6	3.4	379	2	AE2973	hypothetical prote
303	6	3.4	324	2	T20679	376	6	3.4	379	2	P98309	protein kinase (BC
304	6	3.4	325	2	J04950	377	6	3.4	381	1	A60669	protein kinase (BC
305	6	3.4	325	2	TC5276	378	6	3.4	381	1	OKMSR1	benzoate membrane
306	6	3.4	326	2	AD2612	379	6	3.4	383	2	AF3503	hypothetical prote
307	6	3.4	326	2	B97394	380	6	3.4	383	2	P84675	probable membrane
308	6	3.4	327	2	P86813	381	6	3.4	384	2	S64611	alanyl-tRNA synthet
309	6	3.4	329	1	A71511	382	6	3.4	387	2	G97011	alanine racemase (
310	6	3.4	330	2	C83735	383	6	3.4	387	2	H98321	alanine racemase (
311	6	3.4	331	1	A30929	384	6	3.4	388	2	AF2961	hypothetical prote
312	6	3.4	331	2	P85811	385	6	3.4	388	2	H64427	capm protein (capm
313	6	3.4	331	2	AC0752	386	6	3.4	389	2	B71691	major outer membra
314	6	3.4	331	2	P90963	387	6	3.4	389	2	I40864	major outer membra
315	6	3.4	331	2	H64957	388	6	3.4	389	2	D86577	major outer membra
316	6	3.4	331	2	T31779	389	6	3.4	389	2	I40739	alanine racemase (
317	6	3.4	334	2	T29061	390	6	3.4	391	2	H97491	alanine racemase (
318	6	3.4	335	2	C70196	391	6	3.4	391	2	AG2709	isoaspartyl dipept
319	6	3.4	336	2	S06578	392	6	3.4	391	2	AB3791	
320	6	3.4	339	2	B86281	393	6	3.4	391	2	AB3791	
321	6	3.4	339	2	F82896	394	6	3.4	391	2	AB3791	

395	6	3.4	392	2	AH2854	benzoate transport
396	6	3.4	393	2	T04957	hypothetical prote
397	6	3.4	395	2	T23402	conserved hypotnet
398	6	3.4	395	2	A69512	hypothetical prote
399	6	3.4	395	2	B83367	two-component sens
400	6	3.4	396	2	AP2185	hypothetical prote
401	6	3.4	397	2	T25910	pyrimidine nucleos
402	6	3.4	397	2	G70078	hypothetical prote
403	6	3.4	397	2	S74890	conserved hypotnet
404	6	3.4	398	2	D83214	conserved hypotnet
405	6	3.4	399	2	AB3556	alanine racemase (
406	6	3.4	399	2	T30222	senory protein Ki
407	6	3.4	400	2	D83892	transcription regu
408	6	3.4	401	2	I39974	serine proteinase
409	6	3.4	402	2	G71564	hypothetical prote
410	6	3.4	404	2	S42831	F40F12.2 protein -
411	6	3.4	404	2	AB3541	iron-sulfur cluste
412	6	3.4	405	2	AE1002	acetylornithine tr
413	6	3.4	406	2	G86000	acetylornithine de
414	6	3.4	406	2	B91155	acetylornithine de
415	6	3.4	406	2	B65130	acetylornithine tr
416	6	3.4	407	2	C64250	tyrosine- <i>tRNA</i> lig
417	6	3.4	408	2	B90517	conserved hypotnet
418	6	3.4	411	2	S45142	translacton initia
419	6	3.4	411	2	S75327	lysostaphin - <i>Sy</i>
420	6	3.4	413	1	S16426	tyrosine- <i>tRNA</i> lig
421	6	3.4	414	2	T44711	beta-ketoacyl-ACP
422	6	3.4	416	2	AB7116	3-oxoacyl-[acyl]-ca
423	6	3.4	416	2	B69436	5-enolpyruvylshik
424	6	3.4	417	2	T34930	probable secreted
425	6	3.4	419	2	T24820	hypothetical prote
426	6	3.4	419	2	G86517	hypothetical prote
427	6	3.4	420	2	P72103	hypothetical prote
428	6	3.4	420	2	AB4492	probable <i>PtA</i> -like
429	6	3.4	421	2	B72573	probable 3-hydroxy
430	6	3.4	422	2	J80239	lin-10 protein - r
431	6	3.4	422	2	B82676	ABC transporter me
432	6	3.4	423	2	T18784	hypothetical prote
433	6	3.4	425	2	AC3391	tetracenomycin c p
434	6	3.4	425	2	AB4849	probable RING zinc
435	6	3.4	425	2	C97013	probable non-proce
436	6	3.4	426	2	F97552	beta-ketoacyl-ACPs
437	6	3.4	426	2	AH2772	3-oxoacyl- (acyl)-ca
438	6	3.4	426	2	C90425	metabolite transpo
439	6	3.4	426	2	I48379	gene hb protein -
440	6	3.4	427	2	B95046	trigger factor (im
441	6	3.4	427	2	B97917	trigger factor (im
442	6	3.4	428	2	AS3964	carboxyl-terminal
443	6	3.4	428	2	S50646	hypothetical prote
444	6	3.4	428	2	AH3536	dihydroliopamide S
445	6	3.4	430	2	A64880	probable multiple
446	6	3.4	431	1	ZTRC3	citrate utilizatio
447	6	3.4	431	1	ZTRC6	citrate utilizatio
448	6	3.4	431	2	AB6776	histidinol dehydro
449	6	3.4	431	2	E45734	histidinol dehydro
450	6	3.4	431	2	AF0276	probable membrane
451	6	3.4	431	2	T05748	hypothetical prote
452	6	3.4	434	2	AP0585	citrate-proton sym
453	6	3.4	434	2	U00576	citrate carrier pr
454	6	3.4	434	2	S62168	hypothetical prote
455	6	3.4	436	2	B84329	glutamy1- <i>tRNA</i> redu
456	6	3.4	436	2	F69101	phosphomannomutase
457	6	3.4	437	2	F69496	glutamy1- <i>tRNA</i> redu
458	6	3.4	437	2	AB8942	protein R13D11.3 l
459	6	3.4	439	2	B89887	transposase for in
460	6	3.4	439	2	F69216	conserved hypotnet
461	6	3.4	443	2	D95416	probable penicilli
462	6	3.4	444	1	AUBS08	glutamate-ammonia
463	6	3.4	445	2	S65734	mitosis-specific c
464	6	3.4	445	2	AB8956	protein R04F1.3 i
465	6	3.4	446	2	D64210	replicative DNA he
466	6	3.4	446	2	T19625	hypothetical prote
467	6	3.4	446	2	AB3355	hypothetical prote
468	6	3.4	450	2	C75033	adenylosuccinate 1
469	6	3.4	450	2	T38474	serine- <i>tRNA</i> ligase
470	6	3.4	450	2	E72615	probable hysA <i>ABE</i>
471	6	3.4	450	2	H71135	probable adenylosu
472	6	3.4	451	2	T74954	transducer protein
473	6	3.4	451	2	H84479	probable <i>PtA</i> -like
474	6	3.4	451	2	T16418	hypothetical prote
475	6	3.4	452	2	T38962	hypothetical prote
476	6	3.4	452	2	T40634	hypothetical prote
477	6	3.4	453	2	J80155	mitochondrial inne
478	6	3.4	453	2	AB2572	3-phosphoshikimate
479	6	3.4	454	2	T06363	hypothetical prote
480	6	3.4	454	2	AB3555	atrazine chlorohyd
481	6	3.4	457	2	B71476	probable copropor
482	6	3.4	458	2	B64624	GTP-binding protei
483	6	3.4	459	2	S76138	hypothetical prote
484	6	3.4	462	2	E71891	probable GTP bindi
485	6	3.4	463	1	T26378	acid phosphatase (
486	6	3.4	463	1	B83242	probable adenylate
487	6	3.4	464	1	MNVWC	nonstructural prot
488	6	3.4	465	2	A66679	probable RNA-bind
489	6	3.4	466	2	JC6525	processing peptida
490	6	3.4	466	2	AP0190	probable transemb
491	6	3.4	469	2	T49379	citrate synthase,
492	6	3.4	469	2	S41563	citrate (si)-synth
493	6	3.4	469	2	C70961	hypothetical prote
494	6	3.4	469	2	A95396	protein (imported
495	6	3.4	470	2	AB7547	vanillin dehydroge
496	6	3.4	470	2	AE2155	hypothetical prote
497	6	3.4	474	2	T06149	hypothetical prote
498	6	3.4	475	2	A10010	probable membrane
499	6	3.4	475	2	AD1497	Bacillus anthracis
500	6	3.4	480	2	F69505	thymidylate synth
501	6	3.4	481	2	D87696	glutamate synthase
502	6	3.4	482	2	D97152	UDP-N-acetylmuram
503	6	3.4	482	2	S44638	hypothetical prote
504	6	3.4	484	2	F89908	gamma-aminobutylat
505	6	3.4	485	2	A71266	probable transcrip
506	6	3.4	485	2	A39408	crk system potase1
507	6	3.4	486	2	S67589	probable membrane
508	6	3.4	487	2	B82065	RNA polymerase sig
509	6	3.4	487	2	B72755	probable antibioci
510	6	3.4	489	1	A53766	phosphoinositide-s
511	6	3.4	490	1	S44545	SSH1 protein - <i>Yea</i>
512	6	3.4	490	2	S00995	gene twist protein
513	6	3.4	491	2	T48989	hypothetical prote
514	6	3.4	493	2	T27461	hypothetical prote
515	6	3.4	496	2	A47199	1-aminocyclopropan
516	6	3.4	496	2	E72032	general secretion
517	6	3.4	496	2	F86592	uroporhyrin methy
518	6	3.4	496	2	T41114	hypothetical prote
519	6	3.4	496	2	H83592	hypothetical prote
520	6	3.4	497	2	A53373	trpN protein - <i>Pae</i>
521	6	3.4	497	2	F83087	RNA polymerase sig
522	6	3.4	500	2	AH3424	betaine aldehyde d
523	6	3.4	500	2	C81657	general secretion
524	6	3.4	501	2	F71965	lysine- <i>tRNA</i> ligase
525	6	3.4	501	2	F64542	lysine- <i>tRNA</i> ligase
526	6	3.4	501	2	D71499	probable gen. secr
527	6	3.4	502	2	S00720	transcription init
528	6	3.4	502	2	AD0691	conserved hypotnet
529	6	3.4	503	2	B84228	hypothetical prote
530	6	3.4	504	2	AF1789	glucosylate kinase h
531	6	3.4	505	2	C53153	glucose transport
532	6	3.4	505	2	T43154	nitrate transport
533	6	3.4	509	2	AB0683	pyridine nucleotid
534	6	3.4	510	2	AH1811	hypothetical prote
535	6	3.4	511	1	S25707	cytochrome P450 4D
536	6	3.4	511	2	S49151	maturase matk, int
537	6	3.4	511	2	T34315	hypothetical prote
538	6	3.4	512	2	T13611	hypothetical prote
539	6	3.4	512	2	T24032	hypothetical prote
540	6	3.4	512	2	G86459	Hypothetical 55.6

541	6	3.4	513	2	T45624	614	6	3.4	615	2	AP2972	rhizobicin secret
542	6	3.4	513	2	T34546	615	6	3.4	615	2	E98310	rhizobicin secret
543	6	3.4	514	2	A81170	616	6	3.4	617	2	B82285	proteol-export mem
544	6	3.4	514	2	G81935	617	6	3.4	617	2	T29660	hypothetical prote
545	6	3.4	516	2	E96839	618	6	3.4	617	2	B85044	hypothetical prote
546	6	3.4	520	2	AD2383	619	6	3.4	620	2	T10423	estrogen receptor
547	6	3.4	522	2	S41819	620	6	3.4	620	2	H69382	ABC transporter, A
548	6	3.4	523	2	H70886	621	6	3.4	621	1	D69295	endopeptidase la h
549	6	3.4	523	2	T18700	622	6	3.4	621	1	T24090	hypothetical prote
550	6	3.4	524	2	F81207	622	6	3.4	622	2	A45050	transketolase (EC
551	6	3.4	525	2	T20662	623	6	3.4	623	2	P95906	transable adenylate
552	6	3.4	526	2	S03600	624	6	3.4	624	2	A10382	peptidylprolyl iso
553	6	3.4	528	2	T41944	625	6	3.4	625	2	AI0382	topoisomerase IV s
554	6	3.4	528	2	A82256	626	6	3.4	628	2	A82700	hypothetical prote
555	6	3.4	528	2	JC5652	627	6	3.4	629	2	T31798	DNA topoisomerase
556	6	3.4	529	2	D71489	628	6	3.4	632	2	B64127	peptidase PAB1418
557	6	3.4	530	2	F84905	629	6	3.4	632	2	E75057	probable SNF2-type
558	6	3.4	530	2	S46589	630	6	3.4	634	2	S13349	Dnak protein PA476
559	6	3.4	531	2	D83297	631	6	3.4	637	2	B83052	maltoedextrin glyco
560	6	3.4	534	2	JS0173	632	6	3.4	639	2	E72336	beta-glucoside-spe
561	6	3.4	536	2	A34901	633	6	3.4	640	2	AB1423	hypothetical prote
562	6	3.4	536	2	D83419	634	6	3.4	649	2	C81275	phor protein homol
563	6	3.4	539	2	B82393	635	6	3.4	651	2	B84273	leishmanolysin (EC
564	6	3.4	541	2	B46794	636	6	3.4	653	2	A60961	hypothetical prote
565	6	3.4	542	2	B81662	637	6	3.4	653	2	B81277	partial fibrinial u
566	6	3.4	542	2	JQ0201	638	6	3.4	653	2	F85620	membrane protein r
567	6	3.4	544	2	C95854	639	6	3.4	654	2	AB3553	conserved hypothet
568	6	3.4	544	2	S58532	640	6	3.4	660	2	C95287	hypothetical prote
569	6	3.4	548	2	G70610	641	6	3.4	668	2	C71868	hypothetical prote
570	6	3.4	550	2	H64049	642	6	3.4	673	2	AB1936	transcription anti
571	6	3.4	550	2	T22370	643	6	3.4	676	2	AP1153	hypothetical prote
572	6	3.4	554	2	T41612	644	6	3.4	676	2	T40772	hypothetical prote
573	6	3.4	557	1	DWPSUP	645	6	3.4	681	2	C84612	cell-surface molec
574	6	3.4	557	2	T45008	646	6	3.4	682	2	A49121	connectin precurs
575	6	3.4	559	2	E83007	647	6	3.4	682	2	A43318	hypothetical prote
576	6	3.4	559	2	E89134	648	6	3.4	686	2	T08919	hypothetical prote
577	6	3.4	560	2	G72487	649	6	3.4	688	2	S65241	hypothetical prote
578	6	3.4	563	2	A71513	650	6	3.4	688	2	S50580	hypothetical prote
579	6	3.4	566	2	T43456	651	6	3.4	688	2	B42161	CGMP-gated cation
580	6	3.4	567	2	T43463	652	6	3.4	689	2	T08918	hypothetical prote
581	6	3.4	569	2	T20702	653	6	3.4	690	2	B42594	D-amino acid hyd
582	6	3.4	569	2	T00851	654	6	3.4	691	2	D84889	probable ABC trans
583	6	3.4	570	2	C86440	655	6	3.4	692	2	T39154	NADH dehydrogenas
584	6	3.4	570	2	T45712	656	6	3.4	693	2	AB3396	hypothetical prote
585	6	3.4	573	2	T25397	657	6	3.4	694	2	E82783	L-amino-acid oxida
586	6	3.4	574	2	B83388	658	6	3.4	695	2	A38314	probable sensor/re
587	6	3.4	574	2	S48860	659	6	3.4	695	2	AB3375	iron(III) ABC tran
588	6	3.4	575	2	F83904	660	6	3.4	699	2	A83375	transcription init
589	6	3.4	577	2	E71364	661	6	3.4	700	2	H82428	delta-1-pyrroline
590	6	3.4	579	2	T16237	662	6	3.4	704	2	S33263	delta-1-pyrroline-5
591	6	3.4	580	1	A34965	663	6	3.4	717	2	S66637	calpain inhibitor
592	6	3.4	580	1	S15577	664	6	3.4	717	2	T50685	hypothetical prote
593	6	3.4	581	2	F84657	665	6	3.4	718	1	A26615	pyrroline-5-carbox
594	6	3.4	581	2	T31745	666	6	3.4	719	2	T12258	Fe(III)-pyochelin
595	6	3.4	583	2	I50518	667	6	3.4	720	2	A36942	conserved hypothet
596	6	3.4	583	2	T32266	668	6	3.4	721	2	A87128	endo-beta-1,4-glyc
597	6	3.4	583	2	B82744	669	6	3.4	725	2	JC1300	delta-1-pyrroline-
598	6	3.4	585	2	AC3388	670	6	3.4	726	2	T50684	pyrroline-5-carbox
599	6	3.4	586	2	H84966	671	6	3.4	727	2	T08920	hypothetical prote
600	6	3.4	589	1	NDECAS	672	6	3.4	727	2	B83592	hypothetical prote
601	6	3.4	589	2	T32785	673	6	3.4	730	2	H96713	translacton elonga
602	6	3.4	589	2	A34341	674	6	3.4	731	2	S25166	cationic amino aci
603	6	3.4	593	1	KIZPMN	675	6	3.4	736	1	C69451	1,4-alpha-glucan b
604	6	3.4	593	2	I46528	676	6	3.4	741	1	S34218	hypothetical prote
605	6	3.4	593	2	B81277	677	6	3.4	743	1	H96713	hypothetical prote
606	6	3.4	598	2	E72733	678	6	3.4	743	2	T00634	outer layer protei
607	6	3.4	599	2	S15789	679	6	3.4	747	1	VPX845	carbon-monoxide de
608	6	3.4	605	2	C71313	680	6	3.4	747	1	A64319	photoreceptor - De
609	6	3.4	609	2	T27397	681	6	3.4	748	2	D75598	protein P56F3.1 [l
610	6	3.4	609	2	B84783	682	6	3.4	755	2	H88429	1,4-alpha-glucan b
611	6	3.4	611	2	T27820	683	6	3.4	761	2	S47569	hypothetical prote
612	6	3.4	612	2	B95067	684	6	3.4	764	2	T45854	hypothetical prote
613	6	3.4	612	2	A97935	685	6	3.4	769	2		
						686	6	3.4				

687	6	3.4	774	2	T03919	hypothetical prote
688	6	3.4	775	1	VPXR2	outer layer protei
689	6	3.4	776	1	VPXR3	outer layer protei
690	6	3.4	776	1	VPXR1	outer layer protei
691	6	3.4	776	2	S24410	hypothetical outer
692	6	3.4	777	2	S43585	F26F3.1 protein (c
693	6	3.4	794	2	G81177	phosphoenolpyruv
694	6	3.4	794	2	G81927	probable pyruvate,
695	6	3.4	794	2	T37989	DNA mismatch repai
696	6	3.4	795	2	T20609	hypothetical prote
697	6	3.4	801	2	A89862	Na+/H+ antiporter
698	6	3.4	810	2	S75931	hypothetical prote
699	6	3.4	815	2	C71810	type I restriction
700	6	3.4	817	2	C64695	type I restriction
701	6	3.4	818	2	F89819	endonuclease (imp
702	6	3.4	834	1	MMVXPJ	RNA replicase 2 (E
703	6	3.4	834	2	T41568	argonate-like prote
704	6	3.4	834	2	T03369	hypothetical prote
705	6	3.4	834	2	UC8035	N-acetyltransferas
706	6	3.4	836	2	T46070	hypothetical prote
707	6	3.4	839	2	T45908	hypothetical prote
708	6	3.4	844	2	I50159	anion transporter
709	6	3.4	844	2	T32608	hypothetical prote
710	6	3.4	853	2	AD0544	outer membrane fil
711	6	3.4	854	1	XYBYT1	protein N-acetyltr
712	6	3.4	856	2	E75292	GDPBP family prote
713	6	3.4	859	2	AC2089	adenylate cyclase
714	6	3.4	860	2	AB2044	adenylate cyclase
715	6	3.4	862	2	I49583	differentiation an
716	6	3.4	863	2	B72344	tRNA nucleotidyl t
717	6	3.4	866	1	C64834	probable outer mem
718	6	3.4	867	2	T02579	hypothetical prote
719	6	3.4	870	2	T39731	csx2 protein - fis
720	6	3.4	878	2	I51940	gene VAV2 protein
721	6	3.4	881	2	B82097	protein-P-II uridy
722	6	3.4	884	2	T20405	hypothetical prote
723	6	3.4	885	2	S61189	probable membrane
724	6	3.4	891	2	B48642	acortitate hydrat
725	6	3.4	895	2	AD0541	outer membrane fil
726	6	3.4	900	2	A81010	phosphoenolpyruv
727	6	3.4	902	2	T00588	hypothetical prote
728	6	3.4	913	2	E75554	valyl-tRNA synthet
729	6	3.4	916	2	T03323	gene 116 protein -
730	6	3.4	917	2	D81953	phosphoenolpyruv
731	6	3.4	918	2	T21870	hypothetical prote
732	6	3.4	917	2	T02759	hypothetical prote
733	6	3.4	922	2	A30816	band 3 anion trans
734	6	3.4	931	2	B75027	hypothetical prote
735	6	3.4	943	2	S54493	hypothetical prote
736	6	3.4	951	2	D75377	probable proteinas
737	6	3.4	965	2	T09846	phosphoenolpyruv
738	6	3.4	983	2	A38224	protein-tyrosine k
739	6	3.4	1004	2	T38074	hypothetical prote
740	6	3.4	1009	2	B89792	hypothetical prote
741	6	3.4	1020	1	S04200	NAD ADP-ribosyltra
742	6	3.4	1020	1	T29108	hypothetical prote
743	6	3.4	1023	2	B38932	phospholipase C (B
744	6	3.4	1029	2	T18925	hypothetical prote
745	6	3.4	1031	2	H81288	probable sugar tra
746	6	3.4	1034	2	T30331	P-glycoprotein - T
747	6	3.4	1036	2	B96682	hypothetical prote
748	6	3.4	1044	2	G98332	rnd multidrug effl
749	6	3.4	1044	2	AD2950	RND multidrug effl
750	6	3.4	1050	2	H90316	hypothetical prote
751	6	3.4	1051	2	S55259	TfII protein - mou
752	6	3.4	1058	2	S65460	apolipoprotein B -
753	6	3.4	1065	2	A43421	SBCE protein - yea
754	6	3.4	1077	2	A96533	probable zinc meta
755	6	3.4	1086	2	AH1290	cellobiose-phospho
756	6	3.4	1086	2	AT1662	cellobiose-phospho
757	6	3.4	1101	2	T33153	hypothetical prote
758	6	3.4	1103	2	UC4114	Ca2+-transporting
759	6	3.4	1107	2	T25450	hypothetical prote
760	6	3.4	1118	2	T27865	hypothetical prote
761	6	3.4	1132	2	T45037	hypothetical prote
762	6	3.4	1155	2	B96761	probable protein k
763	6	3.4	1157	2	C96761	hypothetical prote
764	6	3.4	1169	2	C84547	hypothetical prote
765	6	3.4	1171	2	T00360	KIA0637 protein -
766	6	3.4	1176	1	A48047	phospholipase C (B
767	6	3.4	1177	2	T16594	hypothetical prote
768	6	3.4	1180	2	A11939	two-component hylr
769	6	3.4	1180	2	A35854	integrin alpha-1 c
770	6	3.4	1188	2	T20333	hypothetical prote
771	6	3.4	1200	2	S77524	chromosome segrega
772	6	3.4	1200	2	C96025	hypothetical expor
773	6	3.4	1208	2	T27832	hypothetical prote
774	6	3.4	1214	2	G70953	probable suca prot
775	6	3.4	1225	2	T39255	probable C2 domain
776	6	3.4	1240	2	S52734	hypothetical prote
777	6	3.4	1259	2	T06521	plittlysin (nc 3.4
778	6	3.4	1260	2	A87046	hypothetical prote
779	6	3.4	1279	2	G86684	prophage pII prote
780	6	3.4	1279	2	T00387	KIA0622 protein -
781	6	3.4	1293	2	S42402	xeroderma pigmento
782	6	3.4	1312	2	T30845	probable DNA repai
783	6	3.4	1314	2	G02870	KIAA0197 protein -
784	6	3.4	1324	2	T00386	hypothetical prote
785	6	3.4	1349	2	T01699	aldehyde oxidase (
786	6	3.4	1355	1	VGBE11	149K glycoprotein
787	6	3.4	1358	2	T01698	aldehyde oxidase (
788	6	3.4	1401	2	T17452	Werner syndrome p
789	6	3.4	1401	2	T30247	Werner syndrome pr
790	6	3.4	1401	2	T39225	MAP kinase kinase
791	6	3.4	1421	2	T00333	hypothetical prote
792	6	3.4	1428	2	T08852	luciferin A - Califo
793	6	3.4	1433	2	B83952	DNA polymerase III
794	6	3.4	1436	2	T14895	DNA helicase I - A
795	6	3.4	1460	1	RNB33L	DNA-directed RNA p
796	6	3.4	1469	1	B36655	slit protein 2 pre
797	6	3.4	1476	2	AC2220	hypothetical prote
798	6	3.4	1480	2	A36665	slit protein 1 pre
799	6	3.4	1488	2	F86428	probable ABC trans
800	6	3.4	1493	2	H71445	hypothetical prote
801	6	3.4	1511	2	T42711	sulfonylurea recep
802	6	3.4	1536	2	A43855	high-molecular-wei
803	6	3.4	1545	2	T42751	sulfonylurea recep
804	6	3.4	1545	2	T46645	sulfonylurea recep
805	6	3.4	1546	2	T42728	sulfonylurea recep
806	6	3.4	1568	2	T09074	semaphorin recepto
807	6	3.4	1570	2	T18272	I-phosphatidylinos
808	6	3.4	1592	2	S63208	hypothetical prote
809	6	3.4	1597	2	S55144	RUB1 protein - yea
810	6	3.4	1648	2	S57163	probable membrane
811	6	3.4	1661	2	S64800	probable membrane
812	6	3.4	1759	2	T03725	replicase polyprot
813	6	3.4	1769	2	S53378	probable membrane
814	6	3.4	1778	2	T50074	adenylate cyclase
815	6	3.4	1839	1	OYBYK	probable nucleopor
816	6	3.4	1847	2	T30558	resistance protein
817	6	3.4	1872	2	UC4976	plexin 3 precursor
818	6	3.4	1884	2	UC4975	plexin 2 precursor
819	6	3.4	1894	2	UC4980	plexin 1 precursor
820	6	3.4	1905	2	S1553	plexin - African c
821	6	3.4	1906	2	AD2443	hypothetical prote
822	6	3.4	1945	2	T13937	plexin A - fruit f
823	6	3.4	1976	2	S56555	sodium channel pro
824	6	3.4	2025	2	D86201	protein F12K11.6 (
825	6	3.4	2051	2	T13164	plexin B - fruit f
826	6	3.4	2052	2	T18290	FYVE finger-contai
827	6	3.4	2114	2	E96505	hypothetical prote
828	6	3.4	2150	2	T08165	RNAI polyprotein -
829	6	3.4	2273	2	T09083	hemagglutinin/hemo
830	6	3.4	2295	2	B71621	probable membrane
831	6	3.4	2348	2	AD1841	hypothetical prote
832	6	3.4	2364	2	I40884	cytotoxin L - C10s

833 6 3.4 2366 2 S10317 toxin B - Clostrid  
834 6 3.4 2367 2 S70172 toxin B - Clostrid  
835 6 3.4 2411 2 A46299 tyrosine kinase su  
836 6 3.4 2411 2 D71623 erythrocyte membra  
837 6 3.4 2459 2 AP2136 peptide synthetase  
838 6 3.4 2528 2 T20719 hypothetical prote  
839 6 3.4 2535 2 T02646 hypothetical prote  
840 6 3.4 2548 2 E59435 myosin IXA (import  
841 6 3.4 2559 2 T30850 fat facets protein  
842 6 3.4 2626 2 T31099 myosin-RhocAP prot  
843 6 3.4 2653 1 S28261 centromere protein  
844 6 3.4 2764 2 T13949 neurofibromin - fr  
845 6 3.4 2802 2 T13945 neurofibromin - fr  
846 6 3.4 2802 2 T13947 neurofibromin - fr  
847 6 3.4 2824 2 T22759 hypothetical prote  
848 6 3.4 2911 2 T20566 hypothetical prote  
849 6 3.4 3119 2 I49729 HD protein - mouse  
850 6 3.4 3163 2 AB0233 yeriniabactin bio  
851 6 3.4 3163 2 T17440 probable polyketid  
852 6 3.4 3429 2 T13853 hypothetical prote  
853 6 3.4 3442 2 E82589 hemagglutinin-like  
854 6 3.4 3455 2 B82519 hemagglutinin-like  
855 6 3.4 3512 2 T17121 CPV protein - midg  
856 6 3.4 3514 2 T19997 hypothetical prote  
857 6 3.4 4427 2 PN0637 polyketide synthas  
858 6 3.4 4639 1 A54794 dynein heavy chain  
859 6 3.4 4644 1 A38905 dynein heavy chain  
860 6 3.4 4717 2 T41581 hypothetical colle

## ALIGNMENTS

RESULT 1  
H83811  
hypothetical protein BH1296 [imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: H83811  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; PMID:20512582; PMID:11058132  
A/Accession: H83811  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-279 <STO>  
A/Cross-references: UNIPROT:Q9KDB7; GB:AF001511; GB:BA000004; NID:G10173727; PIDN:BA050  
A/Experimental source: strain C-125  
C/Genetics:  
A/Gene: BH1296

Query Match 4.5%; Score 8; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFSLISA 13  
DB 13 LAFSLISA 20

RESULT 2  
AC2623  
conserved hypothetical protein Atu0379 [imported] - Agrobacterium tumefaciens (strain C5  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C/Accession: AC2623  
R;Wood, D.M.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCell  
i, Karp, P.; Romero, F.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; PMID:21608550; PMID:11743193  
A/Accession: AC2623  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-305 <KUR>  
A/Cross-references: UNIPROT:Q8UIB8; GB:AE008688; PIDN:AAL41401.1; PID:G17738720; GSPDB:C  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:  
A/Gene: Atu0379  
A/Map position: circular chromosome

Query Match 4.5%; Score 8; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 QAAVVKAL 162  
DB 256 QAAVVKAL 263

RESULT 3  
C97405  
hypothetical protein AGR C 664 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: C97405  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Moliam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.,  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu  
A/Reference number: A97359; PMID:21608551; PMID:11743194  
A/Accession: C97405  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-305 <KUR>  
A/Cross-references: UNIPROT:Q8UIB8; GB:AE007869; PIDN:AAK86196.1; PID:G15155293; GSPDB:C  
C/Genetics:  
A/Gene: AGR C 664  
A/Map position: circular chromosome

Query Match 4.5%; Score 8; DB 2; Length 305;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 QAAVVKAL 162  
DB 256 QAAVVKAL 263

RESULT 4  
T35259  
Probable L-asparagine permease - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: T35259  
R;Oliver, K.; Harrier, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, April 1999  
A/Reference number: Z21573  
A/Accession: T35259  
A/Status: preliminary; translated from GB/EMBL/DDB1  
A/Molecule type: DNA  
A/Residues: 1-489 <OLI>  
A/Cross-references: UNIPROT:Q9X7P0; EMBL:AL049587; PIDN:GAB40684.1; GSPDB:GN00070; SCOE  
A/Experimental source: strain A3 (2)  
C/Genetics:  
A/Gene: SCOE:SCSFA.17  
C/Superfamily: arginine permease

Query Match 4.5%; Score 8; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 VVKALGEL 165  
|||||  
DB 81 VVKALGEL 88

## RESULT 5

T07422  
delta-1-pyrroline-5-carboxylate synthetase - tomato  
CISpecies: Lycopersicon esculentum (tomato)  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: T07422  
R/Magilo, A.; Garcia-Rios, M.; Fujita, T.; Bressan, R.A.; Geonka, L.N.; Jolly, R.U.; Hase  
Proc. ASPP San Antonio Texas 111, 80, 1996  
A>Title: Cloning and partial characterization of PRO2, a second tomato gene encoding the  
A/Reference number: Z16027  
A/Accession: T07422  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-717 <MAQ>  
A/Cross-references: UNIPROT:Q96480; EMBL:U60267; NID:g1480669; PID:g1480670  
C/Genetics:  
A/Gene: PRO2  
C/Function:  
A/Pathway: proline biosynthesis  
C/Superfamily: delta-1-pyrroline-5-carboxylate (P5C) synthetase  
C/Keywords: proline biosynthesis

Query Match 4.5%; Score 8; DB 2; Length 717;  
Best Local Similarity 100.0%; Pred. No. 8.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 108 KISSILANS 115  
|||||  
DB 365 KISSILANS 372

## RESULT 6

response regulator homolog, aerial mycelium formation - Streptomyces griseus  
CISpecies: Streptomyces griseus  
C/Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
C/Accession: A47096  
R/Ueda, K.; Miyake, K.; Horiouchi, S.; Beppu, T.  
J. Bacteriol. 175, 2006-2016, 1993  
A>Title: A gene cluster involved in aerial mycelium formation in Streptomyces griseus et  
A/Reference number: A47096; MUID:93209944; PMID:8458843  
A/Accession: A47096  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-201 <UNB>  
A/Cross-references: UNIPROT:O07640; GB:D13614; NID:g3721543; PIDN:BA43536.1; PID:g30392  
C/Superfamily: response regulator with HTH DNA-binding domain, NatL type; response regul  
C/Keywords: DNA binding; phosphoprotein  
F/54/Binding site: phosphate (Aap) (covalent) #status predicted

Query Match 4.0%; Score 7; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLAFSL 11  
|||||  
DB 128 SLAFSL 134

## RESULT 7

hypothetical protein At2g40380 [imported] - Arabidopsis thaliana  
CISpecies: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: G84828  
R/Lin, X.; Kaul, S.; Rounleley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84828  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-213 <STD>  
A/Cross-references: UNIPROT:Q961Y7; GB:AB002093; NID:g4586054; PIDN:AA025672.1; GSPDB:GN  
C/Genetics:  
A/Gene: At2g40380  
A/Map position: 2  
C/Superfamily: Arabidopsis thaliana hypothetical protein T28U14.50

Query Match 4.0%; Score 7; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 33;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LAFSL 12  
|||||  
DB 90 LAFSL 96

## RESULT 8

JC5710  
TBP-1 interacting protein - mouse  
CISpecies: Mus musculus (house mouse)  
C/Date: 03-Dec-1997 #sequence\_revision 03-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: JC5710  
R/Tanaka, T.; Nakamura, T.; Takagi, H.; Sato, M.  
Biochem. Biophys. Res. Commun. 239, 176-181, 1997  
A>Title: Molecular cloning and characterization of a novel TBP-1 interacting protein (TB  
A/Reference number: JC5710; MUID:98005102; PMID:9345291  
A/Accession: JC5710

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-217 <TAN>  
A/Cross-references: UNIPROT:Q35047; DBJ:AB000121; NID:g2578817; PIDN:BA423155.1; PID:g2

A/Experimental source: testis

C/Comment: This protein is co-localized with Tat binding protein-1 in vivo and enhances

C/Keywords: phosphoprotein

F/200-217/Region: aspartic acid/glutamic acid-rich #status predicted

F/4.28/82/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predict

F/65.163/169/Binding site: phosphate (Tyr) (covalent) #status predicted

F/80.122.155/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status pred

Query Match 4.0%; Score 7; DB 2; Length 217;  
Best Local Similarity 100.0%; Pred. No. 33;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 AAAYKAL 162  
|||||  
DB 45 AAAYKAL 51

## RESULT 9

G70851  
probable gid protein - Mycobacterium tuberculosis (strain H37RV)  
CISpecies: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: G70851  
R/Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A/Reference number: A70500; MUID:98295987; PMID:9634230  
A/Accession: G70851

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-224 <COL>  
A/Cross-references: UNIPROT:O53597; GB:AL021426; GB:AL123456; NID:g3261511; PIDN:CAA1623



A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: gid

Query Match 4.0%; Score 7; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 LRRTSL 71  
|||||  
DB 95 LRRTSL 101

RESULT 10  
C75329  
conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: C75329

R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MWID:20036896; PMID:10567266  
A:Accession: C75329

A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-241 <M1>  
A:Cross-references: UNIPROT:Q9RSX2; GB:AE002038; GB:AE000513; NID:96459790; PIDN:AAF1154

A:Experimental source: strain R1  
C:Genetics:

A:Gene: DR1999  
A:Map position: 1

C:Superfamily: hypothetical protein b1798

Query Match 4.0%; Score 7; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AASLAFS 9  
|||||  
DB 97 AASLAFS 103

RESULT 11

T24485  
hypothetical protein T05A1.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T24485  
R:loyd, C.

submitted to the EMBL Data Library, December 1995  
A:Reference number: Z19897  
A:Accession: T24485

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-251 <M1>  
A:Cross-references: UNIPROT:Q22186; EMBL:Z68219; PIDN:CAA92479.1; GSPDB:GN00022; CESP:TC

A:Experimental source: clone T05A1  
C:Genetics:

A:Gene: CESP:T05A1.7  
A:Map position: 4

A:Introns: 64/2; 107/2; 217/2

Query Match 4.0%; Score 7; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LAFSLUS 12  
|||||  
DB 167 LAFSLUS 173

RESULT 12

T32329  
hypothetical protein C24H12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T32329  
R:Rolling, T.; Wohldmann, P.; Biewald, T.

submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid C24H12.

A:Reference number: Z21151  
A:Accession: T32329

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-260 <R0H>  
A:Cross-references: UNIPROT:O17158; EMBL:AF025451; PIDN:AAF71202.1; GSPDB:GN00020; CESP:

A:Experimental source: strain Bristol N2; clone C24H12  
C:Genetics:

A:Gene: CESP:C24H12.6  
A:Map position: 2

A:Introns: 31/1; 61/2; 109/2; 136/3; 202/3; 226/3  
C:Superfamily: Caenorhabditis elegans hypothetical protein C24H12.6

Query Match 4.0%; Score 7; DB 2; Length 260;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SDIRGSV 53  
|||||  
DB 199 SDIRGSV 205

RESULT 13  
E71674  
hypothetical protein RP682 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii  
C>Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004

C:Accession: E71674  
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Almark, T.

Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MWID:99039499; PMID:9823893  
A:Accession: E71674

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA

A:Residues: 1-293 <AND>  
A:Cross-references: UNIPROT:Q9ZCP1; GB:AJ235272; GB:AJ235269; NID:93861033; PIDN:CAA1511

A:Experimental source: strain Madrid E  
C:Genetics:

A:Gene: RP682  
C:Superfamily: Mg-dependent DNase, TatD type

Query Match 4.0%; Score 7; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ATNLQEI 42  
|||||  
DB 214 ATNLQEI 220

RESULT 14  
A70392  
UDP-glucose-4-epimerase - Aquifex aeolicus

C:Species: Aquifex aeolicus  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C:Accession: A70392  
R:Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O.

V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MWID:98196666; PMID:9537320  
A:Accession: A70392

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-327 <AO>

A:Cross-references: UNIPROT:O67164; GB:AE00721; NID:G2983544; PIDN:AAC07120.1; PID:9298

A:Experimental source: strain VPS

C:Genetics:

A:Gene: galE

C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology F:4-327/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 4.0%; Score 7; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 VKALGE 164

DB 17 VKALGE 23

# RESULT 15

T04262

mitogen-activated protein kinase kinase (EC 2.7.1.-) 1 [similarity] - Arabidopsis thaliana

N:Alternate names: protein F20B18.180

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C:Accession: T04262

R:Bayan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15263

A:Accession: T04262

A:Molecule type: DNA

A:Residues: 1-354 <BEV>

A:Cross-references: UNIPROT:O04440; EMBL:AL049483

A:Experimental source: cultivar Columbia; BAC clone F20B18

C:Genetics:

A:Gene: MAPKK

A:Map position: 4

A:Introns: 24/2; 52/3; 97/3; 172/3; 233/3; 308/2; 323/3

A>Note: F20B18.180

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: phosphotransferase

Query Match 4.0%; Score 7; DB 2; Length 354;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 SSLANSF 116

DB 219 SSLANSF 225

Search completed: November 2, 2005, 19:01:49

Job time : 66 secs